A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24727; GB:J04336; NID:g324000; PIDN:AAA43102.1; PID:g324001
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;18,23,37,53,68,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status pred
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

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Alignment Scores:
Pred. No.:
Score:                 1794.00        Length:          565
Percent Similarity:    98.84%         Matches:         333
Best Local Similarity: 96.80%         Conservative:      7
Query Match:                          Mismatches:        4
DB:                                   Indels:            0
                                      Gaps:              0

US-10-826-929A-1 (1-1061) x HMIVET (1-565)

Qy   30 ATGAAGACAACCATTATTTTGATACTACTGACCATTGGGTCTACAGTCAAAACCCACC 89
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Db    1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy   90 AGTGGAAACAACAGCCACCATTATGTCTGGGACACCAGTAGCAGTAGCAAATGGAACATTG 149
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAlaAsnGlyThrLeu 40

Qy  150 GTAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
         |||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy  210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAATTGCACA 269
         |||||||||||||||||||||||||||||||||:::|||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy  270 TTAATAGATGCAATGCTAGGAGCAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyAlaAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100

Qy  330 CTCTTCATAGAAAGAGAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
         |||||||||||          ||||||||||
Db  101 LeuPheIleGluArgSerAlaSerSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy  390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACCATTAGAATTCACAGCGAGAGGGATTC 449
         ||||||||||||||||||||||||||||||||||||||||||
Db  121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy  450 ACATGGCAGCAGGTGTCACTCAAAACGGAGGAAGTCGAGGCCTGCAAAAAAGGGGATCAGCCGAT 509
         |||||||||||||||||||||||||||||||||||||||||||||
Db  141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160

Qy  510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
         ||||||||||||||||||||||||||||||||||
Db  161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

Qy  570 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGGATTCATCACCCG 629
         ||||||||||||||||||||||||||||||||||||||||||
Db  181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy  630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAGAGCGAGTAACAGTCTCA 689
         ||||||||  :::|||||||||||||||||||||||||||||||
Db  201 SerSerAsnAsnGluGlnThrLysLeuTyrIleGluSerGlyArgValThrValSer 220

Qy  690 ACAAAAAGAAGTCAACAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT 749
         |||||||||||||||||||||||||||||||||||||||||
Db  221 ThrLysArgSerGlnAsnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240
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Qy 750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACTGGAGATATCCAATGATA 809
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         ||||||||||||||||||||:::||::|:|
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Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuIleIle 260

Qy 810 AACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC 869
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         ||||||||||||||||||||||||||:::||
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Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysLysGlyLysSer 280

Qy 870 TCTGTAATGAGATCAGATGACCATAGACATTGTGTCGTGTGAATGTATTACACCAAAT 929
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         |||||||||||||||||||||||||||||
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Db 281 SerValMetArgSerAspAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300

Qy 930 GGAAGCATCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
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         |||||||||||||||||||||||||||||
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Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGATGAGGAATATACCAGAA 1049
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         ||||||||||||||||:::|||
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Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrHisGlyMetArgAsnValProGlu 340

Qy 1050 AAGCAAATCAGA 1061
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Db 341 LysGlnIleArg 344

RESULT 5
HMIVE8
hemagglutinin precursor - influenza A virus (strain A/equine/Santiago/1/85 (H3N8))
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: H34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: H34064
A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24725; GB:J04336; NID:g324016; PIDN:AAA43110.1; PID:g324017
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;18,23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

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Alignment Scores:
Pred. No.:
Score:                 6.55e-140      Length:          565
Percent Similarity:    97.97%         Matches:         327
Best Local Similarity: 95.06%         Conservative:     10
Query Match:           92.47%         Mismatches:        7
DB:                                   Indels:            0
                                      Gaps:              0

US-10-826-929A-1 (1-1061) x HMIVE8 (1-565)

Qy   30 ATGAAGACAACCATTATTTTGATACTACTGACCATTGGGTCTACAGTCAAAACCCAACC 89
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy   90 AGTGGAAACAACAGCCACCATTATGTCTGGGACACCAGTAGCAGTAGCAAATGGAACATTG 149
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAlaAsnGlyThrLeu 40

Qy  150 GTAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
         ||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
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Db   181 ValThrMetProAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy   630 AGCTCAAACCACACGACAGAGAATTGTACATCCAGAATCAGGACGAGTAACAGTCTCA 689
           |||||||| :::||||||||||||||||||||||||||||||
Db   201 SerSerAsnAsnGluGlnThrLysLeuTyrIleGlnAsnGlySerGlyArgValThrValSer 220

Qy   690 ACAAAAGAAGTCAACAAACGATAGTCCCTAATATCGGATCTGGAGATATCCTAATGATA 749
           ||||||| :::|||||||||||| ||:::|||||||||||||||:||||
Db   221 ThrLysArgSerGlnGlnThrIleIleGluProAsnIleGlySerArgProTrpValArgGly 240

Qy   750 ACAGTAATGCCAACTAGTTGCACCGGGCGGGATATTTAAATTGAAAACAGGGAAAAGC 809
           |||||||||||||||||| ||:::||||||||||||||||||||||||||
Db   241 ThrValMetProAsnAsnGlyAsnLeuValAlaProIleIleGlySerArgProTrpValArgGly 260

Qy   810 GGAAGCATCCCAACGACAACACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 869
           ||||||||||||||||||| |||:::||||||||||||||
Db   261 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 280

Qy   870 TCTGTAATGAGATCAGGCGATAAGCATATACTGGACCATTGAAAACCTGGAGATATCCTAATGATA 929
           |||||||||||| ||:::||||||||||||||||||||
Db   281 SerValMetArgSerArgAspAlaProIleAspTyrPheAspLysLeuHisHisPro 300

Qy   930 GGAAGCATCCCAACGACAACACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
           ||||||||||||||||||| |||:::||||||||||||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy   990 CCCAAGTATATCAGGCAAAACAACTTTAAAGGTGGCCACTGGCGATGAGGAATATACCAGAA 1049
           ||||||||||||||||||||:::||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysValAlaThrGlyMetArgAsnValProGlu 340

Qy   1050 AAGCAAATCAGA 1061
           ||||||||||||
Db   341 LysGlnIleArg 344

RESULT 3
S33703
hemagglutinin - influenza A virus H3N8
C;Species: influenza A virus H3N8, equine influenza virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C;Accession: S33703
R;Binns, M.M.; Daly, J.M.; Chirnside, E.D.; Mumford, J.A.; Wood, J.M.; Richards, C.M.;
Arch. Virol. 130, 33-43, 1993
A;Title: Genetic and antigenic analysis of an equine influenza H3 isolate from the 1989
A;Reference number: S33703; MUID:9277383; PMID:8503788
A;Accession: S33703
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-565 <BIN>
A;Cross-references: EMBL:X68437; NID:g312668; PIDN:CAA48482.1; PID:g312669
A;Note: the authors translated the codon ACC for residue 403 as Arg
C;Superfamily: influenza virus hemagglutinin

Alignment Scores:
Pred. No.:   3.61e-142   Length: 565
Score: 1795.00   Matches: 332
Percent Similarity: 99.13%   Conservative: 9
Best Local Similarity: 96.51%   Mismatches: 3
Query Match: 93.88%   Indels: 0
DB: 2   Gaps: 0

US-10-826-929A-1 (1-1061) x S33703 (1-565)

Qy   30 ATGAGAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC 89
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetLysThrThrIleIleIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCATGCAGTAGCAAATGGAACATTG 149
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Db   IleSerGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyAsnCysThr 80
Qy   210 ATTTCAATAGGGAAAATATGCAACAACTCATATAGAGTTCTAGATGGAAGAAATTGCACA 269
           |||||||||||||||||||||||||||||| :::|||||||||||||||||||||||

Qy   270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGATCGTCTTCCAGTATGAGAATTGGGAC 329
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 80

Qy   330 CTCTTCATAGAAGAAGAAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCTGACTAT 389
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerArgAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACCATTAGAATTCACAGCAGAGGGATTC 449
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy   450 ACAATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGAAACTCTTACCCCACATTGAAT 569
           ||||||||||||||||||||||||||||||||||||| |||:::||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProIleLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAAATTCGACAAACTATACATCTGGGGGATTCATCACCCG 629
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy   630 AGCTCAAACCACACGACAGAGAATTGTACATCCAGAATCAGGACGAGTAACAGTCTCA 689
           |||||||| :::||||||||||||||||||||||||||||||
Db   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnAsnGlyArgValThrValSer 220

Qy   690 ACAAAAGAAGTCAACAAACGATAGTCCCTAATATCGGATCTGGAGATATCCTAATGATA 749
           ||||||| :::|||||||||||| ||:::||||||||||||||||:||||
Db   221 ThrGluArgSerGlnGlnThrValIleProAsnIleGlySerArgProTrpValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
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Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

Qy   810 AACAGTAATGCCAACTAGTTGCACCGGGGGATATTTAAATTGAAAACAGGGAAAAGC 869
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Db   261 AsnSerAsnGlyAsnLeuValAlaProIleIleGlySerGlyAsnLysMetIle 280

Qy   870 TCTGTAATGAGATCAGGCGATAAGCATATACTGGACCATTGTGTCTCAGAATGTATTACCAAAT 929
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Db   281 SerValMetArgSerArgAspAlaProIleAspTyrPheAspLysLeuHisHisPro 300

Qy   930 GGAAGCATCCCAACGACAACACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
           |||||||||||||||||||| |||:::||||||||||||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy   990 CCCAAGTATATCAGGCAAAACAACTTTAAAGGTGGCCACTGGCGATGAGGAATATACCAGAA 1049
           |||||||||||||||||||||:::||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysValAlaThrGlyMetArgAsnValProGlu 340

Qy   1050 AAGCAAATCAGA 1061
           ||||||||||||
Db   341 LysGlnIleArg 344

RESULT 4
HMIVET
hemagglutinin precursor - influenza A virus (strain A/equine/Kentucky/2/86[H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: A34065
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: A34065

hemagglutinin precursor - influenza A virus (strain A/equine/Kentucky/1/87[H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: B34065
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169; 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:8204899; PMID:2705299
A;Accession: B34065
A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24728; GB:J04336; NID:g324002; PIDN:AAA43103.1; PID:g324003
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;18,23,37,53,68,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:   Length: 565
Score: 5.27e-143   Matches: 334
Percent Similarity: 1805.00   Conservative: 7
Best Local Similarity: 99.13%   Mismatches: 3
Query Match: 97.09%   Indels: 0
DB: 94.40%   Gaps: 0
                       1

US-10-826-929A-1 (1-1061) x HMIVEE (1-565)

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC 89
          ||||||||||||||||||||::::||||||||||||||||||||||||||||||||||||
Db   1 MetLysThrThrIleIleLeuIleLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy   90 AGTGGAAACAACACAGCCACCATTATGTCTGGGACCACCATGCAGTAGCAAATGGAACATTG 149
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Db   21 SerGlyAsnAsnThrAlaThrIleMetCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy   150 GTAAAAACAATAACTACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy   210 ATTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
          ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy   270 TTAATAGATGCAATGCTAGGAGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnIleTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAAGAAGCAGCCGCTTTCAGCAATTGCTACCCCATATGACATCCCTGACTAT 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGCTCCGGTCCATTGAGCATCCTCAGGAACATTAGAATTCACAGCAGGAGGATTC 449
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Db   121 AlaSerLeuArgSerIleGluHisProGlnGluHisLeuArgIleHisSerArgArgPhe 140

Qy   450 ACATGGACAGGTGTCACTCAAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGGAC 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACCATTGAAT 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerTyrProThrIleGluLeuAsn 180

Qy   570 GTGACAATGCCTAACAAATAAAAATTTCGACAAACTATACATCTCGGGGATTCATCACCCG 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

(left column, rotated)

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 MetLysThrThrIleIleLeuIleLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy   90 AGTGGAAACAACACAGCCACCATTATGTCTGGGACCACCATGCAGTAGCAAATGGAACATTG 149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrIleMetCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy   150 GTAAAAACAATAACTACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
          Db   41 ValLysThrIleThrThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy   210 ATTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
          Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy   270 TTAATAGATGCAATGCTAGGAGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
          Db   81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnIleTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAAGAAGCAGCCGCTTTCAGCAATTGCTACCCCATATGACATCCCTGACTAT 389
          Db   101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGCTCCGGTCCATTGAGCATCCTCAGGAACATTAGAATTCACAGCAGGAGGATTC 449
          Db   121 AlaSerLeuArgSerIleGluHisProGlnGluHisLeuArgIleHisSerArgArgPhe 140

Qy   450 ACATGGACAGGTGTCACTCAAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGGAC 509
          Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACCATTGAAT 569
          Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerTyrProThrIleGluLeuAsn 180

Qy   570 GTGACAATGCCTAACAAATAAAAATTTCGACAAACTATACATCTCGGGGATTCATCACCCG 629
          Db   181 ValThrMetProAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy   630 AGTCAAACCAACACAGCAGACAGAATTGTACATCCAAGAATCAGGAGCGAGTAACAGTCTCA 689
          Db   201 SerSerAsnAsnGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220

Qy   690 ACAAAAAGAAGTCAACAACAACGATAGTCCCTAATATCGGAATCTAGACCGTGGGTTAGGGGT 749
          Db   221 ThrLysArgSerGlnInThrIleIleProAsnIleGlySerArgProValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATA 809
          Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

Qy   810 AACAGTAATGCACAACTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC 869
          Db   261 AsnSerAsnGlyAsnLeuValAlaAlaProArgGlyTyrPheLysLeuArgThrGlyLysSer 280

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTACCACCAAAT 929
          Db   281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300

Qy   930 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
          Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy   990 CCCAGTATATCAGGCAAAAACACTTTAAAGCTGGGATGAGAGGAATATACCAGAA 1049
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Qy   1050 AAGCAAAATCAGA 1061
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Db   341 LysGlnIleArg 344

RESULT 2
HMIVEE

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                    GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:    February 27, 2005, 18:15:54 ; Search time 48 Seconds
                        (without alignments)
                        4253.583 Million cell updates/sec

Title:         US-10-826-929A-1
Perfect score: 1912
Sequence:      1 agcaaaagcagggatatt.........taccagaaaagcaaatcaga 1061

Scoring table:  BLOSUM62
        Xgapop 10.0 , Xgapext  0.5
        Ygapop 10.0 , Ygapext  0.5
        Fgapop  6.0 , Fgapext  7.0
        Delop   6.0 , Delext   7.0

Searched:      283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:    566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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-Q=/cgn2_1/USPTO_spool_p/US1082629/runat_27022005_095243_27596/app.query.fasta_1.1223
-DB=PIR_79 -QFMT=fastan -SUFFIX=pr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US1082629 @CGN_1_1_63 @runat_27022005_095243_27596 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=30 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     PIR_79:*
        1:  pir1:*
        2:  pir2:*
        3:  pir3:*
        4:  pir4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1806	94.5	565	1	HMIVE9	hemagglutinin prec
2	1805	94.4	565	1	HMIVEE	hemagglutinin prec
3	1795	93.9	565	2	S33703	hemagglutinin - in
4	1794	93.8	565	1	HMIVET	hemagglutinin prec
5	1768	92.5	565	1	HMIVE8	hemagglutinin prec
6	1766	92.4	565	1	HMIVE7	hemagglutinin prec
7	1764	92.3	565	1	HMIVE6	hemagglutinin prec
8	1742	91.1	565	1	HMIVE5	hemagglutinin prec
9	1708	89.3	565	1	HMIVE1	hemagglutinin prec
10	1699	88.9	565	1	HMIVE2	hemagglutinin prec
11	1658	86.7	565	1	HMIVE4	hemagglutinin prec
12	1652	86.4	565	1	HMIVE3	hemagglutinin prec
13	1542.5	80.7	566	1	HMIVDU	hemagglutinin prec
14	1538	80.4	550	1	HMIV89	hemagglutinin prec
15	1537	80.4	550	1	HMIV15	hemagglutinin prec
16	1537	80.4	550	1	HMIVS2	hemagglutinin prec
17	1536.5	80.4	566	1	HMIVH	hemagglutinin prec
18	1536	80.3	550	1	HMIV33	hemagglutinin prec
19	1533	80.2	550	2	JQ1153	hemagglutinin prec
20	1530	80.0	550	1	HMIV98	hemagglutinin prec
21	1528	79.9	550	2	JQ1155	hemagglutinin prec
22	1527.5	79.9	566	1	HMIVHA	hemagglutinin prec
23	1525	79.8	550	1	JQ1154	hemagglutinin prec
24	1524	79.7	550	1	HMIV77	hemagglutinin prec
25	1524	79.7	550	1	HMIV80	hemagglutinin prec
26	1514.5	79.2	550	1	HMIV21	hemagglutinin prec
27	1509	78.9	550	2	JQ1156	hemagglutinin prec
28	1501	78.5	550	1	HMIVS3	hemagglutinin prec
29	1479.5	77.4	566	1	HMIVHM	hemagglutinin prec
30	1477.5	77.3	566	1	HMIV6	hemagglutinin prec
31	1472	77.0	567	1	HMIVV	hemagglutinin prec
32	1428	74.7	550	1	HMIV86	hemagglutinin prec
33	1415	74.0	347	2	S52175	hemagglutinin - in
34	1414	74.0	347	2	S52188	hemagglutinin - in
35	1411	73.8	347	2	S52173	hemagglutinin - in
36	1411	73.8	347	2	S52174	hemagglutinin - in
37	1411	73.8	347	2	S52197	hemagglutinin - in
38	1410	73.7	331	2	JQ2378	hemagglutinin - in
39	1410	73.7	331	2	JQ2377	hemagglutinin - in
40	1410	73.7	347	2	S52198	hemagglutinin - in
41	1408	73.6	347	2	S52199	hemagglutinin - in
42	1406.5	73.6	330	2	JQ2375	hemagglutinin - in
43	1406	73.5	347	2	S52176	hemagglutinin - in
44	1404	73.4	347	2	S52183	hemagglutinin - in
45	1404	73.4	347	2	S52182	hemagglutinin - in

ALIGNMENTS

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RESULT 1
HMIVE9
hemagglutinin precursor - influenza A virus (strain A/equine/Tennessee/5/85(H3N8))
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: I34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: I34064
A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24726; GB:J04336; NID:g324020; PIDN:AAA43112.1; PID:g324021
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;18,23,37,53,68,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:               4.35e-143       Length:          565
Score:                   1806.00         Matches:         335
Percent Similarity:      99.13%          Conservative:    6
Best Local Similarity:   97.38%          Mismatches:      3
Query Match:             94.46%          Indels:          0
DB:                      1               Gaps:            0

US-10-826-929A-1 (1-1061) x HMIVE9 (1-565)

Qy          30 ATGAAGACAACAACCATTATTTGATACTACTGACCCATTGGTCTCAGTCAAAACCCAACC 89
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Tue Mar 1 09:55:56 2005

us-10-826-929a-1.rnpb

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Qy    270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGAATGTCTTCCAGTATGAGAATTGGGAC 329
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Qy    330 CTCCTTCATAGAAAGAAGCAGCGCGTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCTTCATAGAAAGAAGCAGCGCGTTTCAGCAGTTGCTACCCATATGACATCCCTGACTAT 360

Qy    390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
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Db    361 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTGGAATTCACAGCAGAGGGATTC 420

Qy    450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
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Db    421 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGATCCTGCAAAAGGGGATCAGCCGAT 480

Qy    510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
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Db    481 AGTTTCTTTAGCCGACTGAATTGGCTAACACAGAATCTGGAAACTCTTACCCCACATTGAAT 540

Qy    570 GTGACAATGCCTAACAATAAAATTTCGACAAACTATACATCTGGGGGATTCATCACCCG 629
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Db    541 GTGACAATGCCTAACAATAAAATTTCGACAAACTATACATCTGGGGGATTCATCACCCG 600

Qy    630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689
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Qy    750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
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Qy    810 AACAGTAATGGCAACTTAGTTGCACCGCGGGGGATATTTTAAATTGAAAACAGGGAAAAGC 869
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    870 TCTGTAATGACATCAGATGCACCCATAGACACATTTGTGTCTCGAATGTATTACACCAAAT 929
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Db    841 TCTGTAATGAGATCAGATGCACCCATAGACACATTTGTGTCTGAATGTATTACACCAAAT 900

Qy    930 GGAAGCATCCCAACGACAAACCATTTCAAATGTGAACAAAGTTACATATGGAAAATGC 989
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Db    901 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 960

Qy    990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGATGAGGAATATACCAGAA 1049
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Qy   1050 AAGCAAATCAGA 1061
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Search completed: March 1, 2005, 08:24:20
Job time : 2066 secs

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RESULT 14
US-10-065-133A-9
; Sequence 9, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT: Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;  LENGTH: 1695
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
US-10-065-133A-9

Query Match             94.6%;  Score 1003.2;  DB 16;  Length 1695;
Best Local Similarity   98.3%;  Pred. No. 3.9e-269;
Matches 1014;  Conservative  0;  Mismatches  18;  Indels  0;  Gaps  0;

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Qy        150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
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Qy        210 ATTTCAATAGGGAAAATATGCAACACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
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Qy        330 CTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCAACATTGCTACCCATAGAATCCCTGACTAT 389
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Qy        390 GCATCGCTCCGGTCACTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
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Qy        450 ACATGCGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGATCAGCCGAT 509
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Db        481 AGTTTCTTTAGCCGACTGAATTGGCTAACAGAATCTGGAAACTCTTACCCACATTGAAT 540

Qy        570 GTGACAATGCCTAACAATAAAATTCGACAAACTATACATCTCGGGGGATTCATCACCCCG 629
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Qy        630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAATCAGTAACAGTCTCA 689
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Qy        690 ACAAAAAGAAGTCAACAAACGATAGTCCCTATATATGGCGATTCAGACCGTGGTTAGGGGT 749
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Qy        750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
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Db        721 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA 780

Qy        810 AACAGTAATGGCAACTTAGTTGCACCGGGATATTTAAATTGAAAACAGGGAAAAGC 869
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Db        781 AACAGTAATGGCAACTTAGTTGCACCGGGATATTTTAAATTGAAAACAGGGAAAAGC 840

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Db        841 TCTGTAATGAGATCAGATGCACCCATAGACATTGTGTGTCGAATGTATTACCACCAAT 900

Qy        930 GGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGAAAATGC 989
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Qy        990 CCCAAGTATATCAGGCAAAAACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA 1049
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RESULT 15
US-10-434-811A-9
; Sequence 9, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;            Education
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT: Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/434,811A
;  CURRENT FILING DATE:  2003-05-08
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;  LENGTH: 1695
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
US-10-434-811A-9

Query Match             94.6%;  Score 1003.2;  DB 17;  Length 1695;
Best Local Similarity   98.3%;  Pred. No. 3.9e-269;
Matches 1014;  Conservative  0;  Mismatches  18;  Indels  0;  Gaps  0;

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Matches 1015;   Conservative 0;   Mismatches 17;   Indels 0;   Gaps 0;

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Db   121 GTAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC   180

Qy   210 ATTTCAATAGGAAAAATATGCAACAACTCATATAAGTTCTGAGATGGAGAAAATTGCACA   269
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Db   181 ATTTCAATAGGAAAAATATGCAACAACTCATATAAGTTCTGAGATGGAGAAAATTGCACA   240

Qy   270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC   329
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Db   241 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC   300

Qy   330 CTCTTCATAGAAAGAAGCAGCGCGTTTCAGCAATTGCTACCCATATGACATCCTGACTAT   389
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTCTTCATAGAAAGAAGCAGCGCGTTTCAGCAGTTGCTACCCATATGACATCCCTGACTAT   360

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTCACAGCAGAGGGATTC   449
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Db   361 GCATCGCTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTCACAGCAGAGGGATTC   420

Qy   450 ACATGGACAGGTGTCACTCAAAACGGAGAAGTGGATCCTGCAAAAGGGAATCAGCCGAT   509
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ACATGGACAGGTGTCACTCAAAACGGAGAAGTGGATCCTGCAAAAGGGAATCAGCCGAT   480

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTGAAT   569
         ||||||||||||||||||||||||||||||
Db   481 AGTTTCTTTAGCCGACTGAATTGGCTAACAGAATCTTGAAACTCTTACCCCACATTGAAT   540

Qy   570 GTGACAATGCCTAACAATAAAAATTCGACAACTATACATCCAAGAATCAGGAGACGAGTCATCACCCG   629
         ||||||||||||||||||||||||||||||||
Db   541 GTGACAATGCCTAACAATAAAAATTTCGACAACTATACATCTCCAAGAATCAGGAGACGAGTCATCACCCG   600

Qy   630 AGCTCAAACCAACCAACAGCAGAGCAGAATTGTCATCCAAGAATCAGGAGACGAGTCTCA   689
         ||||||||||||||||||||||||||||||||
Db   601 AGCTCAAACCAACAAAGAGCAGCAGAAATTGTCATCCAAGAATCAGGAGACGAGTCTCA   660

Qy   690 ACAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGGGATATCCCTAATATGGGGGT   749
         ||||||||||||||||||||||||||||||||
Db   661 ACAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGGGATATCCCTAATATGGGGGT   720

Qy   750 CAATCAGGCCAGGATAAGCAGCATATACTGGACCATTGGAGGAGAATATCCTAATGATA   809
         ||||||||||||||||||||||||||||||||
Db   721 CAATCAGGCCAGGATAAGCAGCATATACTGGACCATTGGAGGAGAATATCCTAATGATA   780

Qy   810 CAATCAGGCCAGGATAAGCAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA   869
         ||||||||||||||||||||||||||||||||
Db   781 CAATCAGGCCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAACGATA   840

Qy   870 TCTGTAATGAGATCAGATGCACCCCATATGAATGCTGGGATATTTGTGTCTGAATGTAATATGGAAAATGC   929
         ||||||||||||||||||||||||||||||||
Db   841 TCTGTAATGAGATCAGATGCACCCCATATGAATGCTGGGATATTTGTGTCTGAATGTAATATGGAAAATGC   900

Qy   930 GGAAGCATCCCAACGTAATGGCCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAACAAAAGGGAAAAGC   989
         ||||||||||||||||||||||||||||||||
Db   901 GGAAGCATCCCAACGACAAACACATTTCAAAATTGAACAAAAGGGAAAAGC   960

Qy   990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA  1049
         ||||||||||||||||||||||||||||||||
Db   961 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATGTACCAGAA  1020

Qy  1050 AAGCAAATCAGA  1061
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Db  1021 AAGCAAATCAGA  1032
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RESULT 13
US-10-872-014-12
; Sequence 12, Application US/10872014
; Publication No. US2004023455A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of   Higher Edu
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/872,014
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/434,811
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/762,861
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-872-014-12

Query Match   94.7%;   Score 1004.8;   DB 18;   Length 1695;
Best Local Similarity 98.4%;   Pred. No. 1.4e-269;

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Db   421 ACATGGACAGGTGTCACTCAAAACGGAGAAGTGGATCCTCGAAAAGGGAATCAGCCGAT   480

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTGAAT   569
         ||||||||||||||||||||||||||||||
Db   481 AGTTTCTTTAGCCGACTGAATTGGCTAACAGAATCTTGAAACTCTTACCCCACATTGAAT   540

Qy   570 GTGACAATGCCTAACAATAAAAATTCGACAACTATACATCCAAGAATCAGGAGACGAGTCTCA   629
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Db   541 GTGACAATGCCTAACAATAAAAATTTCGACAACTATACATCTCCAAGAATCAGGAGACGAGTCTCA   600

Qy   630 AGCTCAAACCAACCAACAGCAGAGCAGAATTGTCATCCAAGAATCAGGAGACGAGTCTCA   689
         ||||||||||||||||||||||||||||||||
Db   601 AGCTCAAACAAAGAGCAGCAGAAATTGTCATCCAAGAATCAGGAGACGAGTCTCA   660

Qy   690 ACAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGGGATATCCCTAATATGGGGGT   749
         ||||||||||||||||||||||||||||||||
Db   661 ACAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGGGATATCCCTAATATGGGGGT   720

Qy   750 CAATCAGGCCAGGATAAGCAGCATATACTGGACCATTGGAGGAGAATATCCTAATGATA   809
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Db   721 CAATCAGGCCAGGATAAGCAGCATATACTGGACCATTGGAGGAGAATATCCTAACGATA   780

Qy   810 AACAGTAATGGCCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAACAAAAGGGAAAAGC   869
         ||||||||||||||||||||||||||||||||
Db   781 AACAGTAATGGCCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAACAAAAGGGAAAAGC   840

Qy   870 TCTGTAATGAGATCAGATGCACCCCATATGAATGCTGGGATATTTGTGTCTGAATGTATTACACCAAAT   929
         ||||||||||||||||||||||||||||||||
Db   841 TCTGTAATGAGATCAGATGCACCCCATATGAATGCTGGGATATTTGTGTCTGAATGTATTACACCAAAT   900

Qy   930 GGAAGCATCCCAACGACCCAACGACAACACCATTTCAAAATGTGAACAAAAGTTACATATGGAAAATGC   989
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Db   901 GGAAGCATCCCAACGACCCAACGACAACACCATTTCAAAATGTGAACAAAAGTTACATATGGAAAATGC   960

Qy   990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA  1049
         ||||||||||||||||||||||||||||||||
Db   961 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATGTACCAGAA  1020

Qy  1050 AAGCAAATCAGA  1061
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Db  1021 AAGCAAATCAGA  1032
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; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 12
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-12

Query Match   94.7%;   Score 1004.8;   DB 17;   Length 1695;
Best Local Similarity   98.4%;   Pred. No. 1.4e-269;
Matches 1015; Conservative   0; Mismatches 17; Indels 0; Gaps   0;

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC 89
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Db   1 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC 60

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCATTGAGAACATTG 149
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Db   61 AGTGGCAACAACACAGCCACATTATGTCTGGGACACCATTGAGAACATTG 120

Qy 150 GTAAAAACAATAACTGATGACCAAATTGAGTGACAAATGCTACTGAATTAGTTCAGAGC 209
        |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db 121 GTAAAAACAATAACTGATGACCAAATTGAGTGACAAATGCTACTGAATTAGTTCAGAGC 180

Qy 210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
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Db 181 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 240

Qy 270 TTAATAGAGTAGCTAGGAGAGACCCCCACTGTGATGTCTTCCAGTGAGTGAAGAATTGGGAC 329
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TTAATAGAGTAGCTAGGAGAGACCCCCACTGTGATGTCTTCCAGTGAGTGAAGAATTGGGAC 300

Qy 330 CTCTTCATAGAGAAGAGAGCAGCGCTTTCAGCAGTGCATCCCATATGACATCCCTGACTAT 389
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Db 301 CTCTTCATAGAGAAGAGAGCAGCGCTTTCAGCAGTGCATCCCATATGACATCCCTGACTAT 360

Qy 390 GCATCGCTTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GCATCGCTTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTCACAGCAGAGGGATTC 420

Qy 450 ACATGGACAGTGTCACTCAAAACGGAAGAAGTGGAGCCTCGAAAAAGGGGATCAGCCGAT 509
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 ACATGGACAGTGTCACTCAAAACGGAAGAAGTGGAGCCTCGAAAAAGGGGATCAGCCGAT 480

Qy 510 AGTTTCTTTAGCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 AGTTTCTTTAGCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 540

Qy 570 GTGACAATGCCTAACATAAAAAATTTCGACAAAACTATACATCGCGGGGATTCATCACCCG 629
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GTGACAATGCCTAACATAAAAAATTTCGACAAAACTATACATCGCGGGGATTCATCACCCG 600

Qy 630 AGCTCAAACCAACACAGCAGAGAATTGTACATCCAAGAATCCGATCGGATCTAGACCTCTCA 689
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AGCTCAAACCAACACAGCAGAGAATTGTACATCCAAGAATCCGATCGGATCTAGACCTCTCA 660

Qy 690 ACAAAAAGAGAGTCAACAACAATAATCCCTAATATCCCTAACATCGGATAGTCCTAATGATA 749
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Db 661 ACAAAAAGAGAGTCAACAACAATAATCCCTAATATCCCTAACATCGGATAGTCCTAATGATA 720

Qy 750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
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Db 721 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAACCATA 780

Qy 810 AACAGTAATGGCAACTTAGTTGCACCCGCGGGATATTTTAAATTGAAAAACAGGGAAAAGC 869
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Db 781 AACAGTAATGGCAACTTAGTTGCACCCGCGGGATATTTTAAATTGAAAAACAGGGAAAAGC 840

Qy 870 TCTGTGTAATGAGATCAGATGCAGCCCCATAGACATTTGTGTGTCTGAATGTATTACACCAAAT 929

Db 841 TCTGTGTAATGAGATCAGATGCAGCCCCATAGACATTTGTGTGTCTGAATGTATTACACCAAAT 900

Qy 930 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 960

Qy 990 CCCAAGTATATCAGGCAAAACACTTTAAAGTGGCCACTGGGATGAGGAATATACCAGAA 1049
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 CCCAAGTATATCAGGCAAAACACTTTAAAGTGGCCACTGGGATGAGGAATGTACCAGAA 1020

Qy 1050 AAGCAAATCAGA 1061
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Db 1021 AAGCAAATCAGA 1032

RESULT 12
US-10-734-373-12
; Sequence 12, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 12
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-12

Query Match   94.7%;   Score 1004.8;   DB 18;   Length 1695;
Best Local Similarity   98.4%;   Pred. No. 1.4e-269;
Matches 1015; Conservative   0; Mismatches 17; Indels 0; Gaps   0;
US-10-734-373-12

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCACC 89
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Db   1 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCACC 60

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCATTGAGAACATTG 149
        ||||| |||||||||||||||||||||||||||||||||||||||||||
Db   61 AGTGGCAACAACACAGCCACATTATGTCTGGGACACCATTGAGAACATTG 120

Qy 150 GTAAAAACAATAACTGATGACCAAATTGAGTGACAAATGCTACTGAATTAGTTCAGAGC 209
        |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db 121 GTAAAAACAATAACTGATGACCAAATTGAGTGACAAATGCTACTGAATTAGTTCAGAGC 180

Qy 210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 240

Qy 270 TTAATAGAGTAGCTAGGAGAGACCCCCACTGTGATGTCTTCCAGTGAGTGAAGAATTGGGAC 329
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Db 241 TTAATAGAGTAGCTAGGAGAGACCCCCACTGTGATGTCTTCCAGTGAGTGAAGAATTGGGAC 300

Qy 330 CTCTTCATAGAGAAGAGAGCAGCGCTTTCAGCAGTTGCTACCCATATGACATCCCTGACTAT 389
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 CTCTTCATAGAGAAGAGAGCAGCGCTTTCAGCAGTTGCTACCCATATGACATCCCTGACTAT 360

Qy 390 GCATCGCTTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTGGAATTGGGAC 449
        ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db 361 ACATGGACAGTGTCACTCAAAAGGAAGAAGTGGAGCCTCGAAAAAGGGGATCAGCCGAT 420

Qy 450 AGTGGAAATGGAACATTG 509

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Db   181  ATTTCAATAGGAAAATATGCAACAACTCATATAGAGTTCTAGAGATGAGGAAGAAATTGCACA  240
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Qy   270  TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTGTGAGAATTGGGAC  329
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Db   241  TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCAGTGTGAGAATTGGGAC  300

Qy   330  CTCTTCATAGAAAAGAAGCAGCGCGCTTTCAGCAATTGCTACCCATATGACATCCTGACTAT  389
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CTCTTCATAGAAAAGAAGCAGCGCGCTTTCAGCAGTTGCTACCCATATGACATCCTGACTAT  360

Qy   390  GCATCGCTCCGGTCCGTCCATTGCTGACATCCTCAGGAACATTAGAATTCACAGCAGAGGATTC  449
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Db   361  GCATCGCTCCGGTCCGTCCATTGCTGACATCCTCAGGAACATTAGAATTCACAGCAGAGGATTC  420

Qy   450  ACATGGACAGTGTCACTCAAAACGGAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT  509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ACATGGACAGTGTCACTCAAAACGGAGAAGTGGATCCTGCAAAAGGGGATCAGCCGAT  480

Qy   510  AGTTTCTTTAGCCGACTGAATTGGTAACAAAATCTTACCCCACATTGAAT  569
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AGTTTCTTTAGCCGACTGAATTGGCTAACAGAATCTGAAACTCTTACCCCACATTGAAT  540

Qy   570  GTGACAATGCCTAACAACAATAAAAATTCGACAAACTATACATCTCGGGGATTCATCACCCG  629
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Db   541  GTGACAATGCCTAACAACAATAAAAATTTCGACAAACTATACATCTCGGGGATTCATCACCCG  600

Qy   630  AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA  689
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Db   601  AGCTCAAACAAAGAGCAGACAAAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA  660

Qy   690  ACAAAAGAGAGTCAACAAACGATAGTCCCTAATATCCCTAACATCCGATCATAGACCGTGGGT  749
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Db   661  ACAAAAGAGAGTCAACAAACAATAATCCCTAACATCCGATCATAGACCGTGGGTCAGGGGT  720

Qy   750  CAATCAGGCAGGATAAGCATAACTACTGACCATTGTAAAACCTGGAGATATCCTAATGATA  809
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Db   721  CAATCAGGCAGGATAAGCATAACTACTGACCATTGTAAAACCTGGAGATATCCTAACGATA  780

Qy   810  AACAGTAATGCAACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC  869
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Db   781  AACAGTAATGCAACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC  840

Qy   870  TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTGTCTGAATGTATTACACCCAAAT  929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  TCTGTAATGAGATCAGATGACCCATAGACATTTGTGTGTCTGAATGTATTACACCCAAAT  900

Qy   930  GGAAGCATCCCCACGACGACAAACCATTTCAAAATGTGAACAAAGTTACACAAAGTGGAAAATGC  989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  GGAAGCATCCCCACGACGACAAACCATTTCAAAATGTGAACAAAGTTACACAAAGTGGAAAATGC  960

Qy   990  CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA  1049
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Qy  1050  AAGCAAATCAGA  1061
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Db  1021  AAGCAAATCAGA  1032
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Qy   601  AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAGCAGAGAATTGTACA  660
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Db   601  AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAAAGAGCAGCAAAATTGTACA  660

Qy   661  TCCAAGAATCAGGACGAGTAACAGTCTGGTAGGGGTCAGGGGTCAACAAACGATAGTCCCTA  720
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Db   661  TCCAAGAATCAGGACGAGTAACAGTCTGGTAGGGGTCAGGGGTCAACAAACGATAATCCCTA  720

Qy   721  ATATCGGATCTAGACCGCGCGGGTCAGGGGTCAATCAGGCAGGATAAGCATAACTACTGGACCA  780
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Db   721  ACATCGGATCTAGACCGCGCGGGTCAGGGGTCAATCAGGCAGGATAAGCATAACTACTGGACCA  780

Qy   781  TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGCAACTTGCACCGCGGGG  840
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Db   781  TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGCAACTTGCACCGCGGGG  840

Qy   841  GATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGACGACCCATAGACA  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  GATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGACGACCCATAGACA  900

Qy   901  TTTGTGTGTCTGAATGTATTACACCAAAATGGAAGCATCCCCACGACGACAAACCATTTCAAA  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TTTGTGTGTCTGAATGTATTACACCAAAATGGAAGCATCCCCACGACGACAAACCATTTCAAA  960

Qy   961  ATGTGAACAAAGTTACATATGGAATATACCAGAAAAGCCCCAAGTATCAGGCAAAAATGCC  1020
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Db   961  ATGTGAACAAAGTTACATATGGAATATACCAGAAAAGCCCCAAGTATCAGGCAAAAATGCC  1020

Qy  1021  TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA  1061
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Db  1021  TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA  1061
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Query Match 94.7%;   Score 1004.8;   DB 16;   Length 1695;
Best Local Similarity 98.4%;
Matches 1015;   Conservative 0;   Mismatches 17;   Indels 0;   Gaps 0;
Pred. No. 1.4e-269;

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Qy    30  ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCACC  89
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCACC  60

Qy    90  AGTGGAAACAACACAGCCACCATTATGTCTGGACACCATGCAGTAGCAAATGGAACATTG  149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AGTGGCAACACACAGCCACCATTATGTCTGGGACACCAGTAGCAAATGGAACATTG  120

Qy   150  GTAAAACAATAACCTGATGACCAAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC  209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC  180

Qy   210  ATTTCAATAGGAAAATATGCAACAACTCATATAAAGTTCTAGAGATGGAAGAAATTGCACA  269
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; Publication No. US2004234553A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher Ed
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT: Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/872,014
;  CURRENT FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/434,811
;  PRIOR FILING DATE: 2003-05-08
;  PRIOR APPLICATION NUMBER: 09/762,861
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 7
;  LENGTH: 1762
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (30)..(1724)
;  OTHER INFORMATION:
US-10-872-014-7

  Query Match             97.3%;  Score 1032.2;  DB 18;  Length 1762;
  Best Local Similarity   98.3%;  Pred. No. 3.2e-277;
  Matches 1043;  Conservative    0;  Mismatches  18;  Indels    0;  Gaps    0;

Qy     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGACAACCATTATTTTGATACTACTGA  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGACAACCATTATTTTGATACCACTGA  60

Qy    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACACAGCCACCATTATGTGTCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACACACAGCCACCATTATGTGTCTGG 120

Qy   121 GACACCATGCAGTAGCAGAAATTGCACATTAATAGATGAACAACTCAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCAGTAGCAGAAATTGCACATTAATAGATGAACAACTCAT 180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAGAGGAAAATGCAACAACTCAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAGAGGAAAATGCAACAACTCAT 240

Qy   241 ATAAAGTTCTAGATGAAGAAATTGCACATTAATAGATGCCTAGGAGACCCCCACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATAGAGTTCTAGATGAAGAAATTGCACATTAATAGATGCCTAGGAGACCCCCACT 300

Qy   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTTCATTGTAGCATCCTCAG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTTCATTGTAGCATCCTCAG 360

Qy   361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCCATTGTAGCATCCTCAG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCCATTGTAGCATCCTCAG 420

Qy   421 GAACATTAGAATTCACAGCAGAGGGATTCACATGACAGGTGTCACTCAAAACGGAAGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAACATTGGAATTCACAGCAGAGGGATTCACATGACAGGTGTCACTCAAAACGGAAGAA 480

Qy   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTAGCCGACTGAATTGGCTAACAA 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGGATCCTGCAAAAGGGGATCAGCCGATAGTTCTTAGCCGACTGAATTGGCTAACAG 540

Qy   541 AATCTGAAAACTCTTACCCCACATTGACAATGCCTAACAATAAAAAATTTCGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AATCTGAAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAAATTTCGACA 600

Qy   601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAGCAGAGGAATTGTACA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAGCAGAGGAACAAAATGTACA 660

Qy   661 TCCAAGAATCAGGACGAGCAGTCTCAACAAAGAAGTCAACAACGATAGTCCCTA 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCCAAGAATCGGGACCAGCAGTCTCAACAAAGAAGTCAACAATAATCCCTA 720

Qy   721 ATATCGGATCTAGACCCTGGGGTTAGGGTCAATGATAAAACAGTAATGGCAACTTAGTTGCACCGCGGG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACATCGGATCTAGACCCGCGGGTCAGGGTCAATGATAAAACAGTAATGGCAACTTAGTTGCACCGCGGG 780

Qy   781 TTGTAAAACCTGGAGATATCCTAATGATAAAACAGGGAAAAGTCTCTGTAATGAGATCAGATGCACCCATAGACA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTGTAAAACCTGGAGATATCCTAATGATAAAACAGGGAAAAGTCTCTGTAATGAGATCAGATGCACCCATAGACA 840

Qy   841 GATATTTTAAATTGAAAACACGGGAAGCATCCCAACAAACCATTCAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GATATTTTAAATTGAAAACACGGGAAGCATCCCAACAAACCATTCAAA 900

Qy   901 TTTGTGTCTGAATGTATTACCACCAAATGGAAGCATCCCAACGACAAACACTTTAAAGC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTTGTGTCTGAATGTATTACCACCAAATGGAAGCATCCCAACGACAAACACTTTAAAGC 960

Qy   961 ATGTGAACAAAGTTACATATGGAAAAATGCCCCAAGTATATCAGGCAAAAACACTTTAAAGC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATGTGAACAAAGTTACATATGGAAAAATGCCCCAAGTATATCAGGCAAAAACACTTTAAAGC 1020

Qy  1021 TGGCCACTGGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
          ||||||||||||||||||||||||||||||||||||||||||
Db  1021 TGGCCACTGGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061
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RESULT 9
US-10-872-014-7
; Sequence 7, Application US/10872014

Qy   1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
          ||||||||||||||||||||||||||||||||||||||||
Db   1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061

RESULT 7
US-10-434-811A-7
; Sequence 7, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-434-811A-7

  Query Match   97.3%; Score 1032.2; DB 17; Length 1762;
  Best Local Similarity   98.3%; Pred. No. 3.2e-277;
  Matches 1043; Conservative   0; Mismatches 18; Indels   0; Gaps   0;

Qy   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACCACTGA 60

Qy   61 CCCATTGGGTCTCACAGTCAAAACCCAACCAGTGAAACAACAACAGCCACCATTATGTCTGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCATTGGGTCTCACAGTCAAAACCCACCAGTGGCAACAACACAGCCACCATTATGTCTCGG 120

Qy   121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGGAAATATGCAACAACTCAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGGAAATATGCAACAACTCAT 240

Qy   241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300

Qy   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGAGCAGCGCTTTCAGCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTGATGTCTTTCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGAGCAGCGCTTTCAGCA 360

Qy   361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG 420

Qy   421 GAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGTGTCACTCAAAACGGAAGAGA 480

Qy   481 GTGGAGCCTGCAAAAGGGGATCAGCCGACTAGTTCTTTTAGCCGACTGAATTGGCTAACA 540
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTCTTAGCCGACTGAATTGGCTAACAG 540

Db   481 GTGGATCCTGCAAAAGGGGATCAGCCGATAGTTCTTCTTAGCCGACTGAATTGGCTAACAG 540

Qy   541 AATCTGGAAACTCTTACCCCACCATGAATGTGACAACATAAAAAATTTCGACA 600
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   541 AATCTGGAAACTCTTACCCCACCATGAATGTGACAACATAAAAAATTTCGACA 600

Qy   601 AACTATACATCTGGGGGATTCATCACCCGAGTCAACAAAAGAGACAGAGAATTGTACA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACTATACATCTGGGGGATTCATCACCCGAGTCAAACAAAAGAGACAGAGAAATTGTACA 660

Qy   661 TCCAAGAATCAGGACAGTAACAGTCTCAACAAAAGAGAGTCAACAAACGATAGTCCCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCCAAGAATCGGGACAGTAACAGTCTCAACAAAAGAGAGTCAACAAACGATAGTCCCTA 720

Qy   721 ATATCGGATCTAGACCCGTGGGTTAGGGGTCAGGGGTCAATCAGGCAGGATAAGCATACTGACCA 780
          | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACATCGGATCTAGACCCGCGGGTCAGGGGTCAATCAGGCAGGATAAGCATATACTGACCA 780

Qy   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840

Qy   841 GATATTTAAATTGAAAACAGGGAAAAGTCTCGTAATGAATGCAGATGACGACCCATAGACA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GATATTTAAATTGAAAACAGGGAAAAGTCTCGTAATGAATGCAGATGACGACCCATAGACA 900

Qy   901 TTTGTGTCGTCTGAATGTATTACACCAAATGGAAGCATCCCAACGACAACAACCATTTCAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTTGTGTCGTCTGAATGTATTACACCAAATGGAAGCATCCCAACGACAACAACCATTTCAA 960

Qy   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTCATATCAGGCGAAAACACTTTAAAGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTCATATCAGGCGAAAACACTTTAAAGC 1020

Qy   1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
          |||||||||||||||||||||| |||||||||||||||||
Db   1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061

RESULT 8
US-10-734-373-7
; Sequence 7, Application US/10734373
; Publication No. US2004013701SA1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-734-373-7

  Query Match   97.3%; Score 1032.2; DB 18; Length 1762;
  Best Local Similarity   98.3%; Pred. No. 3.2e-277;
  Matches 1043; Conservative   0; Mismatches 18; Indels   0; Gaps   0;

Qy   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACCACTGA 60

US-10-065-133A-7

Query Match   97.3%; Score 1032.2; DB 16; Length 1762;
Best Local Similarity 98.3%; Pred. No. 3.2e-277;
Matches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACCACTGA 60

Qy   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACACAGCCACATTATGTCTGG 120
        |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGCAACAACACAGCCACATTATGTCTGG 120

Qy  121 GACACCATGCAGTAGCAGACGGATTCGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GACACCATGCAGTAGCAGACGGATTCGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy  181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240

Qy  241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300

Qy  301 GTGATGTGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GTGATGTGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCA 360

Qy  361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GTTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG 420

Qy  421 GAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAA 480
        ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GAACATTGGAATTCACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAA 480

Qy  481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GTGGATCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAG 540

Qy  541 AATCTGGAAACTCTTACCCACCCACATTGCCTAACAATAAAAAATTTCGACA 600
        |||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  541 AATCTGGAAACTCTTACCCACCCACAATGCCTAACAATAAAAAATTTCGACA 600

Qy  601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACCAGCAGAATTGTACA 660
        |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACAAAGAGCAGCAAAATTGTACA 660

Qy  661 TCCAAGAATCGGGACGAGTAACAGTCTCAACAAAAGAAGTCAACGATAGTCCCTA 720
        ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  661 TCCAAGAATCGGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAACAATAATCCCTA 720

Qy  721 ATATCGGATCTAGAACCGTGGGTTAGGGTGCGCGGCGTCAATCAGCAGGACCA 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ACATCGGATCTAGAACCGTGGGTTAGGGTGCGCGGCGTCAATCAGCAGGACCA 780

Qy  781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840

Qy  841 GATATTTAAATTGAAAACAGGAAAAGCTCTGTGTAATGAGATCAGATGACCCCATAGACA 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GATATTTAAATTGAAAACAGGAAAAGCTCTGTGTAATGAGATCAGATGACCCCATAGACA 900

Qy  901 TTTGTGTGTCTGAATGTATTACACCAAGCATCCCAAGTATATCAGGCAAAACCATTTCAA 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 TTTGTGTGTCTGAATGTATTACACCAAGCATCCCAAGTATATCAGGCAAAACCATTTCAA 960

Qy  961 ATGTGAACAAAGTTACATATATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ATGTGAACAAAGTTACATATATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy 1021 TGGCCACTGGGATGAGGAATGTACCCAGAAAAGCAAATCAGA 1061
        ||||||||||||||||||||||||||||||||||||||||||
Db 1021 TGGCCACTGGGATGAGGAATGTACCCAGAAAAGCAAATCAGA 1061
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RESULT 6
US-10-065-133A-7
; Sequence 7, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:

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;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (30)...(1724)
;  OTHER INFORMATION:
US-10-734-373-10

Query Match       97.4%;  Score 1033.8;  DB 18;  Length 1762;
Best Local Similarity   98.4%;  Pred. No. 1.1e-277;
Matches 1044;  Conservative   0;  Mismatches 17;  Indels   0;  Gaps   0;

Qy    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60

Qy   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACACACAGCCACATTATGTCTGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACACACAGCCACATTATGTCTGG 120

Qy  121 GACACCATGCAGTAGCAGTAACAATGCATTCAGAGCATTTGATGACCAAATTGAGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GACACCATGCAGTAGCAGTAACAATGCATTCAGAGCATTTGATGACCAAATTGAGG 180

Qy  181 TGACAAATGCTACTGAATTAGTTCAGAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TGACAAATGCTACTGAATTAGTTCAGAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240

Qy  241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300

Qy  301 GTGATGTCTTCCAGTAGTGGAGAATTGGGACCTCTTCATGAGAAAGAAGCAGCGCTTTCAGCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GTGATGTCTTCCAGTAGTGGAGAATTGGGACCTCTTCATGAGAAAGAAGCAGCGCTTTCAGCA 360

Qy  361 ATTGCTACCCATATGACATCCCTGACTATGGCATCGCTCCGGTCCATGTCATCCTCAG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GTTGCTACCCATATGACATCCCTGACTATGGCATCGCTCCGGTCCATGTCATCCTCAG 420

Qy  421 GAACATTAGAATTCACAGCAGAGGGATTCACATGACAGTGTCACTCAAAACGGAAGAA 480
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Db  421 GAACATTGGAATTCACAGCAGAGGGATTCACATGACAGTGTCACTCAAAACGGAAGAA 480

Qy  481 GTGGAGCCTGCAAAAGGGGATCAGCCGAGTAGTTCTTTAGCCGACTGAATTGGCTAACA 540
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Db  481 GTGGATCCTGCAAAAGGGGATCAGCCGAGTAGTTCTTTAGCCGACTGAATTGGCTAACAG 540

Qy  541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGAAAATTTCGACA 600
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Db  541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGAAAATTTCGACA 600

Qy  601 AACTATACATCTCGGGAGATTCATCACCCGAGCTCAAAACAGCAGAATTGTACA 660
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Db  601 AACTATACATCTCGGGAGATTCATCACCCGAGCTCAAAACAGCAGAATTGTACA 660

Qy  661 TCCAAGAATCAGGACGAGTAACGATGCAACAATAATCCCTA 720
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Db  661 TCCAAGAATCAGGACGAGTAACGATGCAACAATAATCCCTA 720

Qy  721 ATATCGGATCTAGACCGTGGGTTAGGGTCAGGCAGGATAAGCATATACTGGACCA 780
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Db  721 ACATCGGATCTAGACCGTGGGTTCAGGGGTCAGGCAGGATAAGCATATACTGGACCA 780

Qy  781 TTGTAAAACCTGGAGATATCCTAATGATAAAACAGTAATGCCAACTTAGTTGCACCGGGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TTGTAAAACCTGGAGATATCCTAACGATAAAACAGTAATGCCAACTTAGTTGCACCGGGG 840

Qy  841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGCAATGCAGATGACCCATAGACA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGCAATGCAGATGACCCATAGACA 900

Qy  901 TTTGTGTGTCTGAATGTATTACACCAAATGAAGCATCCCAACGACAAAACCATTTCAAA 960
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Db  901                                                            960
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Qy  961 ATGTGAACAAGTTACATATGGAATGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ATGTGAACAAGTTACATATGGAATGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy 1021 TGGCCACTGGGATGGAGGAGGATATACCAGAAAAGCAAATCAGA 1061
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RESULT 5
US-10-872-014-10
; Sequence 10, Application US/10872014
; Publication No. US20040234553A1
; GENERAL INFORMATION:
;  APPLICANT: The University of Pittsburgh - of the Commonwealth System of    Higher Edu
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT: Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C1-PUS-1
;  CURRENT APPLICATION NUMBER: US/10/872,014
;  CURRENT FILING DATE:   2004-06-18
;  PRIOR APPLICATION NUMBER: 10/434,811
;  PRIOR FILING DATE:   2003-05-08
;  PRIOR APPLICATION NUMBER: 09/762,861
;  PRIOR FILING DATE:   2001-08-24
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE:   1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE:   1998-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;  LENGTH: 1762
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (30)...(1724)
;  OTHER INFORMATION:
US-10-872-014-10

Query Match       97.4%;  Score 1033.8;  DB 18;  Length 1762;
Best Local Similarity   98.4%;  Pred. No. 1.1e-277;
Matches 1044;  Conservative   0;  Mismatches 17;  Indels   0;  Gaps   0;

Qy    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60
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Db    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60

Qy   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACACACAGCCACATTATGTCTGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACACACAGCCACATTATGTCTGG 120

Qy  121 GACACCATGCAGTAGCAGTAACAATGCATTCAGAGCATTTGATGACCAAATTGAGG 180
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Db  121 GACACCATGCAGTAGCAGTAACAATGCATTCAGAGCATTTGATGACCAAATTGAGG 180

Qy  181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
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Qy  241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
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Qy  301 GTGATGTCTTCCAGTAGTGGACCTCTTCATGAGAAAGAAGCAGCGCTTTCAGCA 360
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Db  301 GTGATGTCTTTCAGTAGTGGACCTCTTCATGAGAAAGAAGCAGCGCTTTCAGCA 360

Qy  361 ATTGCTACCCATATGACATCCCTGACTATGCGGTCCGGTCCATGTCATCCTCAG 420
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Qy    301  GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCA  360
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Db    301  GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCA  360

Qy    361  ATTGCTACCCATTGACATCCCTGACTATGCATCCTCCGGTCATTGTAGCATCCTCAG     420
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Db    361  GTTGCTACCCATTGACATCCCTGACTATGCATCCTCCGGTCATTGTAGCATCCTCAG     420

Qy    421  GAACATTAGAATTCACAGCAGAGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA    480
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Db    421  GAACATTGGAATTCACAGCAGAGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA    480

Qy    481  GTGAGCCTGCAAAGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA     540
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Db    481  GTGGATCCTGCAAAGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAG    540

Qy    541  AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCTAACAATAACAATAAAATTTCGACA    600
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Db    541  AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCTAACAATAACAATAAAATTTCGACA    600

Qy    601  AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGAATTGTACA    660
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Db    601  AACTATACATCTGGGGATTCATCACCCGAGCTCAAACAAGAGCAGACAAAATTGTACA    660

Qy    661  TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGTCAACAAGATAGTCCCTA    720
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Db    661  TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGTCAACAAACAATAATCCCTA    720

Qy    721  ATATCGGATCTAGACCGTGGGTTAGGGTCAGGATAAGCATATACTGGACCA    780
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Db    721  ACATCGGATCTAGACCGTGGGTCAGGGTCAGGATAAGCATATACTGGACCA    780

Qy    781  TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGCCAACTTAGTTGCACCGCGGG    840
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Db    781  TTGTAAAACCTGGAGATATCCTAACGATAAACAGTAATGCCAACTTAGTTGCACCGCGGG    840

Qy    841  GATATTTTAAATTGAAAACAGGGAAAGCTCTGTAATGAGATCAGCATCCCAACGACAAACCATTTCAAA    900
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Db    841  GATATTTTAAATTGAAAACAGGGAAAGCTCTGTAATGAGATCAGCATCCCAACGACAAACCATTTCAAA    900

Qy    901  TTTGTGTGTCTGAATGTATTACACCAAATGAAGCATCCCAAGTATATCAGGCAAACACTTTAAAGC    960
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Db    901  TTTGTGTGTCTGAATGTATTACACCAAATGAAGCATCCCAAGTATATCAGGCAAACACTTTAAAGC    960

Qy    961  ATGTGAACAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAACACTTTAAAGC   1020
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Db    961  ATGTGAACAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAACACTTTAAAGC   1020

Qy   1021  TGGCCACTGGGATGGGAATGAGGAAATATACCAGAAAAAGCAAATCAGA   1061
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RESULT 4
US-10-734-373-10
; Sequence 10, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762

RESULT 3
US-10-434-811A-10
; Sequence 10, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-434-811A-10

Query Match   97.4%; Score 1033.8; DB 17; Length 1762;
Best Local Similarity   98.4%; Pred. No. 1.1e-277;
Matches 1044; Conservative   0; Mismatches   17; Indels   0; Gaps   0;

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Qy    61  CCCATTGGGTCTCACAGTCAAAACCCAACCAGTGGAAACAACACAGCCACATTATGTCTGG   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  CCCATTGGGTCTCACAGTCAAAACCCAACCAGTGGCAACAACACAGCCACATTATGTCTGG   120

Qy   121  GACACCATGCAGTAGCAAATGACAAATTGGTAAAAACAATAACTAACTGATGACCAAATTGAGG   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GACACCATGCAGTAGCAAATGACAAATTGGTAAAAACAATAACTAACTGATGACCAAATTGAGG   180

Qy   181  TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGAAAATATGCAACAACTCAT   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGAAAATATGCAACAACTCAT   240

Qy   241  ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGGACCCCCACT   300
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Db   241  ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGGACCCCCACT   300
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Query Match   97.4%;   Score 1033.8;   DB 16;   Length 1762;
Best Local Similarity   98.4%;   Pred. No. 1.1e-277;
Matches 1044;   Conservative   0;   Mismatches 17;   Indels   0;   Gaps   0;

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Db 121 GACACCATGCAGTAGCAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG   180

Qy 181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGGAAAATATGCAACAACTCAT 240
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Db 181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGGAAAATATGCAACAACTCAT 240

Qy 241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCACT   300
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Qy 421 GAACATTAGAATTCACAGCAGAGGATTCACATGACAGGTGTCACTCAAACGGAAGAA   480
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Db 421 GAACATTAGAATTCACAGCAGAGGATTCACATGACAGGTGTCACTCAAACGGAAGAA   480

Qy 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCACGGGG   540
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Db 541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAATTCGACA   600

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Db 601 AACTATACATCTGGGGATTCATCACCCGAGCTCAACCAACAGCAGACAGAATTGTACA   660

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Db 661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTA   720

Qy 721 ATATCGGATCTAGACCGTCTGGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780
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Db 721 ATATCGGATCTAGACCGTCTGGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780

Db 121 GACACCATGCAGTAGCAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG   180

Qy 181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGGAAAATATGCAACAACTCAT 240
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Db 181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGGAAAATATGCAACAACTCAT 240

Qy 241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCACT   300
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Db 241 ATAGAGTTCTAGATGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCACT   300

Qy 301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAGAAGCAGCGCTTTCAGCA   360
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Db 301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAGAAGCAGCGCTTTCAGCA   360

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Qy 421 GAACATTAGAATTCACAGCAGAGGATTCACATGACAGGTGTCACTCAAACGGAAGAA   480
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Qy 481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCACGGGG   540
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Qy 661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTA   720
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Qy 721 ATATCGGATCTAGACCGTCTGGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780
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Qy 781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGCAACTTAGTTGCACCGCGGG   840
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Qy 841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA   900
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Qy 901 TTTGTGTGTCTGAATGTATTACACCAAAATGGAAGCATCCCCAAGCACAAACACTTTCAAA 960
Db 901 TTTGTGTGTCTGAATGTATTACACCAAAATGGAAGCATCCCCAAGCACAAACACTTTCAAA 960

Qy 961 ATGTGAACAAAGTTACATATGGGAATATACCAGAAAATGCCCCAAGTATCAGGCAAAATCAGA 1020
Db 961 ATGTGAACAAAGTTACATATGGGAATATACCAGAAAATGCCCCAAGTATCAGGCAAAATCAGA 1020

Qy 1021 TGGCCACTGGGATGGAGAGGAATATACCAGAGAAAGCAAATCAGA   1061
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Post-processing: Minimum Match 0%
Maximum Match 100%
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Score	Query Match	Match Length	DB	ID	Description
1	1061	100.0	1061	19	US-10-826-929A-1	Sequence 1, Appl
2	1033.8	97.4	1762	16	US-10-065-133A-10	Sequence 10, Appl
3	1033.8	97.4	1762	17	US-10-434-811A-10	Sequence 10, Appl
4	1033.8	97.4	1762	18	US-10-734-373-10	Sequence 10, Appl
5	1033.8	97.4	1762	18	US-10-872-014-10	Sequence 10, Appl
6	1032.2	97.3	1762	16	US-10-065-133A-7	Sequence 7, Appli
7	1032.2	97.3	1762	17	US-10-434-811A-7	Sequence 7, Appli
8	1032.2	97.3	1762	18	US-10-734-373-7	Sequence 7, Appli
9	1032.2	97.3	1762	18	US-10-872-014-7	Sequence 7, Appli
10	1004.8	94.7	1695	16	US-10-065-133A-12	Sequence 12, Appl
11	1004.8	94.7	1695	17	US-10-434-811A-12	Sequence 12, Appl
12	1004.8	94.7	1695	18	US-10-734-373-12	Sequence 12, Appl
13	1004.8	94.7	1695	18	US-10-872-014-12	Sequence 12, Appl
14	1003.2	94.6	1695	16	US-10-065-133A-9	Sequence 9, Appli
15	1003.2	94.6	1695	17	US-10-434-811A-9	Sequence 9, Appli
16	1003.2	94.6	1695	18	US-10-734-373-9	Sequence 9, Appli
17	1003.2	94.6	1695	18	US-10-872-014-9	Sequence 9, Appli
18	607.2	57.2	1777	9	US-09-918-568-54	Sequence 54, Appl
19	125.2	11.8	1711	13	US-10-099-619-1	Sequence 1, Appli
20	124.2	11.7	1775	18	US-10-855-875-7	Sequence 7, Appli
21	123.6	11.6	1733	17	US-10-397-635-13	Sequence 13, Appl
22	122.4	11.5	1110	18	US-09-918-568-57	Sequence 57, Appl
23	105.4	9.9	1754	9	US-09-918-568-27	Sequence 27, Appl
24	98.2	9.3	1728	9	US-09-918-568-28	Sequence 28, Appl
25	96.6	9.1	1783	9	US-09-918-568-46	Sequence 46, Appl
26	94.8	8.9	1683	19	US-10-617-569-2	Sequence 2, Appli
27	92.8	8.7	1647	18	US-10-839-509-3	Sequence 3, Appli
28	91.8	8.7	1773	18	US-10-381-530-4	Sequence 4, Appli
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32	74.8	7.0	329	9	US-09-918-568-41	Sequence 41, Appl
33	72.6	6.8	334	9	US-09-918-568-40	Sequence 40, Appl
34	48.8	4.6	1135	9	US-09-918-568-49	Sequence 49, Appl
35	48.6	4.6	424	9	US-09-918-568-31	Sequence 31, Appl
36	48.6	4.6	429	9	US-09-918-568-32	Sequence 32, Appl
37	47	4.4	424	9	US-09-918-568-30	Sequence 30, Appl
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40	40.8	3.8	116792	13	US-10-087-192-1090	Sequence 1090, Ap
c 41	40.6	3.8	442	9	US-09-918-568-29	Sequence 29, Appl
c 42	40.2	3.8	8866	14	US-10-239-676-140	Sequence 140, App
c 43	40.2	3.8	8866	15	US-10-240-453-154	Sequence 154, App
c 44	38.6	3.6	81748	13	US-10-087-192-364	Sequence 364, App
c 45	38.6	3.6	253861	18	US-10-741-601-5611	Sequence 5611, Ap

ALIGNMENTS

RESULT 1
US-10-826-929A-1
; Sequence 1, Application US/10826929A
; Publication No. US2005003272A1
; GENERAL INFORMATION:
; APPLICANT: Lai, Alexander
; TITLE OF INVENTION: DNA Vaccine Expressing HA1 of Equine-2 Influenza Virus
; FILE REFERENCE: 57657/04-265
; CURRENT APPLICATION NUMBER: US/10/826,929A
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/470,843
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1061
; TYPE: DNA
; ORGANISM: A/Eq/Kentucky/98
US-10-826-929A-1

Query Match 100.0%; Score 1061; DB 19; Length 1061;
Best Local Similarity 100.0%; Pred. No. 2.2e-285;
Matches 1061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 GACACCATGCAGTAGCAGTAGGCAAATGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
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RESULT 15
US-10-065-133A-12
; Sequence 12, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT: Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/065,133A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;  LENGTH: 1695
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
US-10-065-133A-12

Query Match          94.7%;  Score 1004.8;  DB 4;  Length 1695;
Best Local Similarity  98.4%;  Pred.No. 2.2e-294;
Matches 1015;  Conservative   0;  Mismatches  17;  Indels   0;  Gaps   0;

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Qy    870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTACCACCAAAT 929
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Search completed: March  1, 2005, 06:18:12
Job time : 223 secs
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Query Match   94.7%; Score 1004.8; DB 4; Length 1695;
Best Local Similarity 98.4%; Pred. No. 2.2e-294;
Matches 1015; Conservative   0; Mismatches 17; Indels   0; Gaps   0;

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RESULT 14
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; Sequence 12, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-12

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;   CLASSIFICATION:  424
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Frommer, William S.
;   REGISTRATION NUMBER:  25,506
;   REFERENCE/DOCKET NUMBER:  454310-2740
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:   (212) 840-3333
;   TELEFAX:   (212) 840-0712
;   INFORMATION FOR SEQ ID NO:  300:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1762 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
US-08-458-101-300

Query Match          96.0%;  Score 1018.4;  DB 1;  Length 1762;
Best Local Similarity 97.5%;  Pred. No. 1.7e-298;
Matches 1034;  Conservative  0;  Mismatches  27;  Indels  0;  Gaps  0;

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Qy  121  GACACCAGTAGCAATGGCAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG  180
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Db  601  AACTATACATCTGGGGGATTCATCACCCGACGCTCAAACCAACAGCAGCAAAATTGTATA  660

Qy  661  TCCAAGAATCAGGACGAGTAACAGTTCTCAACAAAAGAGAGTCAACAAACGATAGTCCCTA  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  TCCAAGAATCAGGACGAGTAACAGTTCTCAACAAAAGAGAGTCAACAAACAGTAATCCCTA  720

Qy  721  ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA  780
         |||||||| |||||||||||||||||||||||||||||||||||||||||
Db  721  ACATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA  780

Qy  781  TTGTAAAACCTGGAGATATTCTAACGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG  840
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Db  781  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TTGTAAAACCTGGAGATATTCTAACGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG  840

Qy  841  GATATTTTAAATTGAAAACAGGAGAAAGCTCTGTAATGGATGCAGATGCACCCATAGACA  900
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  841  GATATTTTAAATTGAACAGAACAGGAGAAAGCTCTGTAATGGATGCAGATGCACCCATAGACA  900

Qy  901  TTTGTGTCTGAATGTATTACCACCAAATGGAAGCATCCCAACGACAAAACCATTTCAAA  960
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  901  CTTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCAACGACAAAACCATTTCAAA  960

Qy  961  ATGTGAACAAAGTTACATATGAGAAAATGCCCCAAGTATATCAGGAAAACACTTTAAAGC  1020
         |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  961  ATGTGAACAAAGTTACATATGAGAATGGAAAATGCCCCAAGTATATCAGGAAAACACTTTAAAGC  1020

Qy 1021  TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA  1061
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Db 1021  TGGCCACCGGGATGAGGAATGTACCAGAAAAGCAAATCAGA  1061
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RESULT 13
US-09-506-286B-12
; Sequence 12, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;   APPLICANT:  Dowling, Patricia W.
;   APPLICANT:  Youngner, Julius S.
;   APPLICANT:  The University of Pittsburgh, of the Commonwealth
;   TITLE OF INVENTION:  COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;   FILE REFERENCE:  EQ-1-C2
;   CURRENT APPLICATION NUMBER:  US/09/506,286B
;   CURRENT FILING DATE:  2000-02-16
;   PRIOR APPLICATION NUMBER:  09/133,921
;   PRIOR FILING DATE:  1998-08-13
;   PRIOR APPLICATION NUMBER:  PCT/US99/18583
;   PRIOR FILING DATE:  1999-08-12
;   NUMBER OF SEQ ID NOS:  108
;   SOFTWARE:  PatentIn Ver. 2.1
;   SEQ ID NO 12
;   LENGTH:  1695
;   TYPE:  DNA
;   ORGANISM:  Equine influenza virus_H3N8
US-09-506-286B-12

Query Match          94.7%;  Score 1004.8;  DB 4;  Length 1695;
Best Local Similarity 98.4%;  Pred. No. 2.2e-294;
Matches 1015;  Conservative  0;  Mismatches  17;  Indels  0;  Gaps  0;

Qy   30  ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAACCCAACC   89
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Db    1  ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAACCCAACC   60

Qy   90  AGTGGAAACAACACAGCCACCATTATGTCTGGACACCAGTAGCAATGGCAACATTG  149
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Db   61  AGTGGCAACAACACAGCCACCATTATGTCTGGACACCAGTAGCAATGGCAACATTG  120

Qy  150  GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC  209
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC  180

Qy  210  ATTTCAATAGGGAAAATATGCAACACTCATATAAAGTTCTAGATGATGGAATGGAAGAA  269
         ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db  181  ATTTCAATAGGGAAAATATGCAACACTCATATAAAGTTCATAGATGATGGAATGGAAGAA  240

Qy  270  TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGCAATTGCAACAATTGCACA  329
         ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGCAATTGCAACAATTGCACA  300

Qy  330  CTCTTCATGATAGAAAGAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCCTGACTACTAT  389
         |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  301  CTCTTCATGAAAGAGGAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCCTGACTACTAT  360

Qy  390  GCATCGCCTCCGTCCATTGTAGCATCCTCAATGATAAACAGTAATAGAATTCACAGCAGAGGGATTC  449
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          ;   STATE:  NY
          ;   COUNTRY:  USA
          ;   ZIP:  10036
          ; COMPUTER READABLE FORM:
          ;   MEDIUM TYPE:  Floppy disk
          ;   COMPUTER:  IBM PC compatible
          ;   OPERATING SYSTEM:  PC-DOS/MS-DOS
          ;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
          ; CURRENT APPLICATION DATA:
          ;   APPLICATION NUMBER:  US/08/709,209
          ;   FILING DATE:  21-AUG-1996
          ;   CLASSIFICATION:  424
          ; PRIOR APPLICATION DATA:
          ;   APPLICATION NUMBER:  US 08/105,483
          ;   FILING DATE:  12-AUG-1993
          ;   APPLICATION NUMBER:  US 07/847,951
          ;   FILING DATE:  06-MAR-1992
          ; ATTORNEY/AGENT INFORMATION:
          ;   NAME:  Frommer, William S.
          ;   REGISTRATION NUMBER:  25,506
          ;   REFERENCE/DOCKET NUMBER:  454310-2400
          ; TELECOMMUNICATION INFORMATION:
          ;   TELEPHONE:  (212) 840-3333
          ;   TELEFAX:  (212) 840-0712
          ; INFORMATION FOR SEQ ID NO:  300:
          ;   SEQUENCE CHARACTERISTICS:
          ;   LENGTH:  1762 base pairs
          ;   TYPE:  nucleic acid
          ;   STRANDEDNESS:  single
          ;   TOPOLOGY:  linear
          US-08-709-209-300

Query Match        96.0%;   Score 1018.4;   DB 1;  Length 1762;
Best Local Similarity   97.5%;   Pred. No. 1.7e-298;
Matches 1034;  Conservative   0;  Mismatches  27;  Indels   0;  Gaps   0;

Qy      1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60
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Db      1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60

Qy     61 CCGATTGGGTCTACAGTCAAAACCCACCAGTGGAAACAACACAGCCACATTATGTCTGG 120
            ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCCATTGGGTCTACAGTCAAAACCCACCAGTGGCAACACACAGCCACATTATGTCTGG 120

Qy    121 GACACCACGAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACACCACGAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy    181 TGACAAATGCTACTGAATTAGTTCAGAGCATTCAATAGGGAAAAATGCAACAACTCAT 240
            ||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db    181 TGACAAATGCTACTGAATTAGTTCAGAGCATTCAATAGGGAAAAATGCAACAATCCAT 240

Qy    241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATAGGGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300

Qy    301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAGAGCAGCGGCTTTCAGCA 360
            |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGATGTTTTTCNGTATGAGAATTGGGACCTCTTCATAGAAAGAGAGCAGCGGCTTTCAGCA 360

Qy    361 ATTGCTACCCATATGACATCCCGACTATGCATCGCTCCGGTCCGTCCGTGAGCATCCTCAG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTGCTACCCATATGACATCCCGACTATGCATCGCTCCGGTCCGTCCGTGAGCATCCTCAG 420

Qy    421 GAACATTAGAATTCACAGCAGAGGGATTCACATGACAGGTGTCACTCAAAACGGAAGAA 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GAACATTAGAATTCACAGCAGAGGGATTCACATGACAGGTGTCACTCAAAACGGAAGAA 480

Qy    481 GTGGAGCCGTCGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540

Qy    541 AATCTGGAAACTCTTACCCCACATTGAAATGTGACAATGCCTAACAATAAAAAATTTCGACA 600
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Db    541 AATCTGGAAATTCTTACCCCATATTGAAATGTGACAATGCCTAACAACCACAGCAGCAGAATTTCGATA 600

Qy    601 AACTATACATCTGGGGGGATTCATCACCGAGCTCAACAACCAAAAGCAGCAGAATTGTACA 660
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    601 AACTATACATCTGGGGGGATTCATCACCGAGCTCAAACAAAAGAGCAGCAAAAATTGTATA 660

Qy    661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACGTAGTCCCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAGAAAAGAAGTCAACAGTAATCCCTA 720

Qy    721 ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGGCAGGATATAAGCATATACTGGACCA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACATCCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCAGGATATAAGCATATACTGGACCA 780

Qy    781 TTGTAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGGCGGG 840
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    781 TTGTAAACCTGGAGATATTCTAACGATAAACAGTAATGGCAACTTAGTTGCACCGGCGGG 840

Qy    841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGCGCACCCATAGACA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GATATTTTAAATTGAGAACAGGGAAAAGCTCTGTAATGAGATCAGATCAGCGCACCCATAGACA 900

Qy    901 TTTGTGTGTCTGAATGTATTACACCAAATGAAGCATCCCAACGACAAAAACCATTTCAAA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTTGTGTGTCTGAATGTATTACCACAAATGAAGCATCCCAACGACAAAAACCATTTCAA 960

Qy    961 ATGTGAACAAAGTTACATATGAAAAATGCCCCAAGTATATCAGGCAAAAGCAAATCAGA 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGTGAACAAAGTTACATATGAAAAATGCCCCAAGTATATCAGGCAAAAGCAAATCAGA 1020

Qy   1021 TGGCCACTGGGATGAGGAGAATATACCAGAAAGCAAATCAGA 1061
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Db   1021 TGGCCACCGGGGATGAGGAGAATGTACCAGAAAGCAAATCAGA 1061
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RESULT 12
US-08-458-101-300
; Sequence 300, Application US/08458101
; Patent No. 5766599
; GENERAL INFORMATION:
;   APPLICANT:  Paoletti, Enzo
;   APPLICANT:  Perkus, Marion E.
;   APPLICANT:  Taylor, Jill
;   APPLICANT:  Tartaglia, James
;   APPLICANT:  No. 5766599ton, Elizabeth K.
;   APPLICANT:  Riviere, Michel
;   APPLICANT:  de Taisne, Charles
;   APPLICANT:  Limbach, Keith J.
;   APPLICANT:  Johnson, Gerard P.
;   APPLICANT:  Pincus, Steven E.
;   APPLICANT:  Cox, William I.
;   APPLICANT:  Audonnet, Jean-Christophe Francis
;   APPLICANT:  Gettig, Russell Robert
;   TITLE OF INVENTION:  GENETICALLY ENGINEERED VACCINE
;   TITLE OF INVENTION:  STRAIN
;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Curtis, Morris & Safford
;     ADDRESSEE:  c/o William S. Frommer
;     STREET:  530 Fifth Avenue
;     CITY:  New York
;     STATE:  NY
;     COUNTRY:  USA
;     ZIP:  10036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/458,101
;     FILING DATE:  01-JUN-1995
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Db   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAAATATGCAACAATCCAT 240

Qy   241 ATAAAGTTCTGAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCCACT 300
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Db   241 ATAGGGTTCTGAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCACT 300

Qy   301 GTGATGTCTTCAGTATGAGAATTGGGACCTCTTCATAGAAGAGCAGGGCTTTCAGCA 360
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Db   301 GTGATGTTTTCNGTATGAGAATTGGGACCTCTTCATAGAAGAGCAGGGCTTTCAGCA 360

Qy   361 ATTGCTACCCATATGACATCCCTGACTATGCATGCTCCGGTCCATTGTAGCATCCTCAG 420
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Db   361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCCGGTCCATTGTAGCATCCTCAG 420

Qy   421 GAACATTAGAATTCACAGCAGAGGGATTCACATGACAGGTGTCACTCAAAACGGAAGAA 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAACATTAGAATTCACAGCAGAGGGATTCACATGACAGGTGTCACTCAAAACGGAAGAA 480

Qy   481 GTGGAGCCTGCAAAAGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA 540
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Db   481 GTGGAGCCTGCAAAAGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA 540

Qy   541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATTTCGACA 600
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Db   541 AATCTGGAAATTCTTACCCCATATTGAATGTGACAATGCCTAACAATAAAAATTTCGATA 600

Qy   601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGAGAATGTACA 660
             ||||||||||||||||||||||||||||||||| ||||||||||||||||| ||||
Db   601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAAAATGTATA 660

Qy   661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAAGAGTCAACAAACGATAGTCCCTA 720
             |||||||||||||||||||||||||||||||| |||||||||||| || ||||||||
Db   661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAGAAAGAGTCAACAAACGTAATCCCCTA 720

Qy   721 ATATCGGATCTAGACCGTGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780
             || |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   721 ACATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780

Qy   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTGTCACGCGGG 840
             ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   781 TTGTAAAACCTGGAGATATTCTAACGATAAACAGTAATGCAACTTAGTGTCACGCGGG 840

Qy   841 GATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGGACTCAGATGCACCCATAGACA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GATATTTAAATTGAACACAGGGAAAAGCTCTGTAATGGACTCAGATGCACCCATAGACA 900

Qy   901 TTTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAACGACAAAACCATTTCAAA 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CTTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAACGACAAAACCATTTCAAA 960

Qy   961 ATGTGAACAAAGTTACATATGGACAAAAAGCCCCAAGTATATCAGGCAAAAACACTTTAAAGC 1020
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Db   961 ATGTGAACAAAGTTACATATGGAATAATGCCCCAAGTATATCAGGCAAAAACACTTTAAAGC 1020

Qy  1021 TGGCCACTGGGATGGAGGAATATACCAGAAAAGCAAATCAGA 1061
             ||||||||||||||||||||||||||||||||||||||||||
Db  1021 TGGCCACCGGGATGGAGGAATGTACCAGAAAAGCAAATCAGA 1061
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RESULT 11
US-08-709-209-300
; Sequence 300, Application US/08709209
; Patent No. 5762938
; GENERAL INFORMATION:
;   APPLICANT: Paoletti, Enzo
;   TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
;   TITLE OF INVENTION: STRAIN
;   NUMBER OF SEQUENCES: 462
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Curtis, Morris & Safford
;   ADDRESSEE: c/o William S. Frommer
;   STREET: 530 Fifth Avenue
;   CITY: New York

```
Db   901 GGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAATGCCTGGCCACTGGGATGGAGGAATATACCAGAA 960

Qy   990 CCCAAGTATATCAGCAAAAACACTTTAAAGCTGGCCACTGGGATGGAGGAATATACCAGAA 1049
             ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   961 CCCAAGTATATCAGCCAAAAACACTTTAAAGCTGGCCACTGGGATGGAGGAATGTACCAGAA 1020

Qy  1050 AGCAAATCAGA 1061
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Db  1021 AGCAAATCAGA 1032
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RESULT 10
US-08-105-483-300
; Sequence 300, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
;   APPLICANT: Paoletti, Enzo
;   TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
;   TITLE OF INVENTION: STRAIN
;   NUMBER OF SEQUENCES: 462
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Curtis, Morris & Safford
;   ADDRESSEE: c/o William S. Frommer
;   STREET: 530 Fifth Avenue
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10036
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/105,483
;   FILING DATE: 12-AUG-1993
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/847,951
;   FILING DATE: 06-MAR-1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Frommer, William S.
;   REGISTRATION NUMBER: 25,506
;   REFERENCE/DOCKET NUMBER: 454310-2400
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 840-3333
;   TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 300:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1762 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-105-483-300

Query Match   96.0%; Score 1018.4; DB 1; Length 1762;
Best Local Similarity 97.5%; Pred. No. 1.7e-298;
Matches 1034; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
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Qy     1 AGCAAAAGCAGGGGATATTCTGTCAATCATGAGAGCAACCATTATTTTGATACTACTGA 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGCAAAAGCAGGGGATATTCTGTCAATCATGAGAGCAACCATTATTTTGATACTACTGA 60

Qy    61 CCCATTGGGTCTCACAGTAGCAAATGGCAAACCCAACCAGTCGAAACAACAGCCACCATTATGTCTCGG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCCATTGGGTCTCACAGTAGCAAATGGCAAACCCAACCAGTCGCAACAACAGCCACCACATTATGTCTCGG 120

Qy   121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCAGTAGCGAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAAATATGCAACAACTCAT 240
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; SOFTWARE:    PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Equine Influenza Virus, Newmarket 2/93 Strain
US-09-622-951-1

Query Match          96.1%;    Score 1019.2;    DB 4;    Length 1698;
Best Local Similarity  99.2%;    Pred. No. 9.5e-299;
Matches 1024;    Conservative 0;    Mismatches 8;    Indels 0;    Gaps 0;

Qy      30 ATGAGAGACAACCATTATTTGATACATCGGGCTCACAGTCAAAACCCACC 89
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Db       1 ATGAGAGACAACCATTATTTGATACATCGGGCTCACAGTCAAAACCCACC 60

Qy      90 AGTGGAAACAACACAGCCACATTATGTCGGGACACCAGTAGCAACATTG 149
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Db      61 AGTGGCAACAACACAGCCACATTATGTCGGGACACCAGTAGCAACATTG 120

Qy     150 GTAAAACAATAACTGATGACCAAATTGAGTGACAAATGCTACTGAGTTCAGAGC 209
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Db     121 GTAAAACAATAACTGATGACCAAATTGAGTGACAAATGCTACTGAGTTCAGAGC 180

Qy     210 ATTTCAATAGGGAAAATATGCAACACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATTTCAATAGGGAAAATATGCAACACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 240

Qy     270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 300

Qy     330 CTCTTCATAGAAAGAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCTTCATAGAAAGAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 360

Qy     390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGACAGGAATTCACAGCAGAGGGGATTC 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGACAGGAATTCACAGCAGAGGGGATTC 420

Qy     450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTCGAAAAGGGGATCAGCCGAT 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTCGAAAAGGGGATCAGCCGAT 480

Qy     510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTGGAAACTCTTACCCCACATTGAAT 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTGGAAACTCTTACCCCACATTGAAT 540

Qy     570 GTGACAAATGCCTAACAATAAAAATTTCGACAACTATACATCTCGGGGATTCATCACCCG 629
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GTGACAAATGCCTAACAATAAAAATTTCGACAACTATACATCTCGGGGATTCATCACCCG 600

Qy     630 AGCTCAAACCAACACAGCAGAGAATTGTACATCCAAGAATCAGGAGAATCAGAGTAACAGTCTCA 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGCTCAAACCAACACAGCAGAGAATTGTACATCCAAGAATCAGGAGAATCAGAGTAACAGTCTCA 660

Qy     690 ACAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTCCTGAGATATCCTAATGATA 749
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ACAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTCCTGAGATATCCTAATGATA 720

Qy     750 CAATCAGGCAGGAGGATAAGCATATATGGACCATTGTGAAAACCTGGAGATATCCTAATGATA 809
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CAATCAGGCAGGAGGATAAGCATATATGGACCATTGTGAAAACCTGGAGATATCCTAATGATA 780

Qy     810 AACAGTAATGCCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAAAACAGGGAAAAGC 869
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AACAGTAATGCCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAAAACAGGGAAAAGC 840

Qy     870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCGTAATGTATTACACCAAAT 929
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCGTAATGTATTACACCAAAT 900

Qy     930 GGAAGCATCCCAACGACAACAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     181 TGACAAATGCTACTGAGTTCAGAGCCATTCAATAATGCAACAACTCAT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||
Qy     241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCACT 300
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCACT 300

Qy     301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAGCAGCGCTTTCAGCA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAGCAGCGCTTTCAGCA 360

Qy     361 ATTGCTACCCATATGACATCGCTCCGGTCCATTGTGAGCATCCTCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTTGCTACCCATATGACATCGCTCCGGTCCATTGTGAGCATCCTCAG 420

Qy     421 GAACATTAGAATTCACAGCAGAGGGATTCACAGACAGTGTCACTCAAAACGGAAGAA 480
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Db     421 GAACATTAGAATTCACAGCAGAGGGATTCACAGACAGTGTCACTCAAAACGGAAGAA 480

Qy     481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GTGGATCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAG 540

Qy     541 AATCTTGGAAACTCTTACCCCACATTGAATGTGACAATGAATGTGACAATGCCTAACAATAATCCCTA 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AATCTTGGAAACTCTTACCCCACATTGAATGTGACAATGAATGTGACAATGCCTAACAATAATCCCTA 600

Qy     601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACAACAGCAGAGAATTGTACA 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACAACAGCAGAGAATTGTACA 660

Qy     661 TCCAAGAATCAGGAGGACGAGTAACAGTCTCAACAAAGAAGAGTCAACAAACGATAGTCCCTA 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TCCAAGAATCAGGAGGACGAGTAACAGTCTCAACAAAGAAGAGTCAACAAACAATAATCCCTA 720

Qy     721 ATATCCGGATCCTAGACCCGGGGTCAGGGTAGGGGTCAATCAGGCAGGAGGATAAGCATATATGGACCA 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ACATCGGATCCTAGACCCGGGGTCAGGGTAGGGGTCAATCAGGCAGGAGGATAAGCATATATGGACCA 780

Qy     781 TTGTGTCGTCTGAGATATCCTAATGATAAACAGTAATGCCAACTTAGTTGCACCGGGG 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTGTGTCGTCTGAGATATCCTAATGATAAACAGTAATGCCAACTTAGTTGCACCGGGG 840

Qy     841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGACCCCATAGACA 900

Qy     901 TTTGTGTCGTCTGAATGTATTACACCAAATGCCCCAAGCATCCCCAACGACAACAAACCATTTCAA 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TTTGTGTCGTCTGAATGTATTACACCAAATGCCCCAAGCATCCCCAACGACAACAAACCATTTCAA 960

Qy     961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCGCAAAACACTTTAAAGC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCGCAAAACACTTTAAAGC 1020

Qy    1021 TGGCCACTGGAGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
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Db    1021 TGGCCACTGGAGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
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RESULT 9
US-09-622-951-1

; Sequence 1, Application US/09622951
; Patent No. 6713068
; GENERAL INFORMATION:
;   APPLICANT: JEAN CHRISTOPHE AUDONNET ET AL.
;   TITLE OF INVENTION: LIVE RECOMBINED VACCINES INJECTED WITH ADJUVANT
;   FILE REFERENCE: 454313-3159
;   CURRENT APPLICATION NUMBER: US/09/622,951
;   CURRENT FILING DATE: 2000-10-17
;   PRIOR APPLICATION NUMBER: PCT/FR99/00453
;   PRIOR FILING DATE: 1999-03-01
;   NUMBER OF SEQ ID NOS: 31

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; GENERAL INFORMATION:
;   APPLICANT: Dowling, Patricia W.
;   APPLICANT: Youngner, Julius S.
;   TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;   FILE REFERENCE: EQ-1-C2-1
;   CURRENT APPLICATION NUMBER: US/10/065,133A
;   CURRENT FILING DATE: 2002-12-10
;   PRIOR APPLICATION NUMBER: PCT/US99/18583
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 09/133,921
;   PRIOR FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 108
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1762
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (30)...(1724)
;   OTHER INFORMATION:
US-10-065-133A-7

  Query Match             97.3%;  Score 1032.2;  DB 4;  Length 1762;
  Best Local Similarity   98.3%;  Pred. No. 1.1e-302;
  Matches 1043;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60
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Db     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACCACTGA 60

Qy    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACAACAGCCACATTATGTCTGG 120
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Db    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACACACAGCCACATTATGTCTGG 120

Qy   121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGTACA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGTACA 180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTCAATAATGATGCAACAACTCAT 240
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Db   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTCAATAATGATGCAACAACTCAT 240

Qy   241 ATAAAGTTCTAGATGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATAGAGTTCTAGATGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300

Qy   301 GTGATGTCTTCCAGTGATGAGAATTGGGACCTCTTCATAGAAAGAAGAGCAGCGCTTTCAGCA 360
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Db   301 GTGATGTCTTCAGTGATGAGAATTGGGACCTCTTCATAGAAAGAAGAGCAGCGCTTTCAGCA 360

Qy   361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCGGTTGAGCATCCTCAG 420
         |||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCGGTTGAGCATCCTCAG 420

Qy   421 GAACATTAGAATTCACAGCAGAGGATTCACATGACAGTGTCACTCAAAACGGAAGAA 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAACATTAGAATTCACAGCAGAGGATTCACATGACAGTGTCACTCAAAACGGAAGAA 480

Qy   481 GTGGAGCCTGCAAAAGGGGGATCAGCCGACTGAGTTCTTTAGCCGACTGGCTAACAG 540
         ||||||||| |||||||||| ||||||||||||||||||||||||||||||
Db   481 GTGTGATCCTGCAAAAGGGGGATCAGCCGACTGAGTTCTTTAGCCGACTGGCTAACAG 540

Qy   541 AATCTGGAAACTCTTACCCCCACATTGAATGCTAACAATAAAAATTTCGACCA 600
         |||||||||||| |||||||||||||||||||||||||||||||||||||
Db   541 AATCTGGAAACTCTTACCCCACATTGAATGCTAACAATAAAAATTTCGACCA 600

Qy   601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGAATTGTACA 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGAATTGTACA 660

Qy   661 TCCAAGAATCGGGACGACGAGTAACAGTCTCAACAAAAGAGAGTCCCTA 720
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Db   661 TCCAAGAATCGGGACGAGTAACAGTCTCAACAAAAGAGAGTCACAAACAATAATCCTA 720

Qy   721 ATATCGGATCTAGACCGTGGGTTAGGGTGTCAATCAGGCAGGATAAGCATATACTGACCA 780
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Db   721 ACATCGGATCTAGACCGCGGGTCAGGGTCAATCAGGCAGGATAAGCATATACTGACCA 780

Qy   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840

Qy   841 GATATTTAAATTGAAAACAGGGAGAAAGTCTCGTAATGAGATCAGATGCACCCATAGACA 900
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Db   841 GATATTTAAATTGAAAACAGGGAGAAAGTCTCGTAATGAGATCAGATGCACCCATAGACA 900

Qy   901 TTTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAAGCACAAACCATTTCAAA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   901 TTTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAAGCACAAACCATTCAAA 960

Qy   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy  1021 TGGCCACTGGGATGAGGAATACCAGAAAAGCAAATCAGA 1061
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Db  1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061


RESULT 8
US-10-434-811A-7
; Sequence 7, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
;   APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;   APPLICANT: Education
;   APPLICANT: Dowling, Patricia W.
;   APPLICANT: Youngner, Julius S.
;   TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;   FILE REFERENCE: EQ-1-C1-PUS-1
;   CURRENT APPLICATION NUMBER: US/10/434,811A
;   CURRENT FILING DATE: 2003-05-08
;   PRIOR APPLICATION NUMBER: PCT/US99/18583
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 09/133,921
;   PRIOR FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1762
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (30)...(1724)
;   OTHER INFORMATION:
US-10-434-811A-7

  Query Match             97.3%;  Score 1032.2;  DB 4;  Length 1762;
  Best Local Similarity   98.3%;  Pred. No. 1.1e-302;
  Matches 1043;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60
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Db     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACCACTGA 60

Qy    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACACACACCGCCACATTATGTCTGG 120
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACACACAGCCACATTATGTCTGG 120

Qy   121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAATGATGCAACAACTCAT 240
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Qy   61 CCCATTGGGTCTACAGTCAAAACCCACCAGTGGAAACAACACAGCGCCACATTATGTCTGG 120
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Db   61 CCCATTGGGTCTACAGTCAAAACCCACCAGTGGAAACAACACAGCGCCACATTATGTCTGG 120

Qy 121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy 181 TGACAAATGCTACTGAATTAGTTCAGAGCATTCAATAGGGAAAATATGCAACAACTCAT 240
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Db 181 TGACAAATGCTACTGAATTAGTTCAGAGCATTCAATAGGGAAAATATGCAACAACTCAT 240

Qy 241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACACCCCACT 300
         |||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db 241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACACCCCACT 300

Qy 301 GTGATGTCTTCCAGTATGACGAATTGGACCTCTCATAGAAAGAAGCAGCGCTTTCAGCA 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GTGATGTCTTTCAGTATGACGAATTGGACCTCTCATAGAAAGAAGCAGCGCTTTCAGCA 360

Qy 361 ATTGCTACCCATATGACATCATCCCTGACTATGCATGCTCCGTCCGTTCACTCAAAACGGAAGAA 420
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Db 361 GTTGCTACCCATATGACATCATCCCTGACTATGCATGCTCCGTCCGTTCACTCAAAACGGAAGAA 420

Qy 421 GAACATTAGAATTCACAGCAGAGGGATTCAGCCGATAGTTTCTTAGCCGACTGAATTGGCTAACAA 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 GAACATTGGAATTCACAGCAGAGGGATTCAGCCGATAGTTTCTTAGCCGACTGAATTGGCTAACAA 480

Qy 481 GTGGAGCCTGCAAAAGGGATCAGCCGATAGTTTCTTAGCCGACTGAATTGGCTAACAG 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GTGGATCCTGCAAAAGGGATCAGCCGATAGTTTCTTAGCCGACTGAATTGGCTAACAG 540

Qy 541 AATCTGGAAACTCTTACCCACCATTGAATGTGACAATGCCTAACATAAAAAATTTCGACA 600
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Db 541 AATCTGGAAACTCTTACCCACCATTGAATGTGACAATGCCTAACATAAAAAATTTCGACA 600

Qy 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAACACAGCAGAATTGTACA 660
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Db 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAACACAGCAGAATTGTACA 660

Qy 661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAACGATAGTCCCTA 720
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Db 661 TCCAAGAATCGGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAACAATAATCCCTA 720

Qy 721 ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGGTCAGGATAAGCATATACTGGACCA 780
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Db 721 ACATCCGGATCTAGACCGCGGGTCAGGGTCAATCAGGATAAGCATATACTGGACCA 780

Qy 781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840

Qy 841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAATGAGATCAGATGCACCCATAGACA 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAATGAGATCAGATGCACCCATAGACA 900

Qy 901 TTTGTGTGTCTGAAATGTATTACCAAGTGAAGCATCCCCAAGTATCAGGCAAAACTTTAAAGC 960
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Db 901 TTTGTGTGTCTGAAATGTATTACCAAGTGAAGCATCCCCAAGTATCAGGCAAAACTTTAAAGC 960

Qy 961 ATGTGAACAAAGTTACATATGGAAAATGCCCAGTATATCAGGCAAAACACTTTAAAGC 1020
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Db 961 ATGTGAACAAAGTTACATATGGAAAATGCCCAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy 1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
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Db 1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061

RESULT 7
US-10-065-133A-7
; Sequence 7, Application US/10065133A
; Patent No. 6685946

Db 541 AATCTGGAAACTCTTACCCACCATTGAATGTGACAATGCCTAACATAAAAAATTTCGACA 600

Qy 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAACACAGCAGAATTGTACA 660
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Db 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAACACAGCAGAATTGTACA 660

Qy 661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAACGATAGTCCCTA 720
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Db 661 TCCAAGAATCGGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAACAATAATCCCTA 720

Qy 721 ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGGTCAGGATAAGCATATACTGGACCA 780
         ||||| ||||||||||| |||| ||||||||||||||||||||||||||||||||||||
Db 721 ACATCCGGATCTAGACCGCGGGTCAGGGTCAATCAGGATAAGCATATACTGGACCA 780

Qy 781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
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Db 781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840

Qy 841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAATGAGATCAGATGCACCCATAGACA 900
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Db 841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAATGAGATCAGATGCACCCATAGACA 900

Qy 901 TTTGTGTGTCTGAAATGTATTACACCAACCATTCAAA 960
         ||||||||||||||||||||||||||||||||||||
Db 901 TTTGTGTGTCTGAAATGTATTACACCAACCATTCAAA 960

Qy 961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
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Db 961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy 1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
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Db 1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061

RESULT 6
US-09-762-861B-7
; Sequence 7, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HK2-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1999-08-12
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-09-762-861B-7

Query Match   97.3%; Score 1032.2; DB 4; Length 1762;
Best Local Similarity 98.3%; Pred. No. 1.1e-302;
Matches 1043; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy   1 AGCAAAAGCAGGGGATATTTCGTCAATCATGAAGACAACAACCATTATTTTGATACTACTGA 60
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Db   1 AGCAAAAGCAGGGGATATTTCGTCAATCATGAAGACAACAACCATTATTTTGATACCACTGA 60

Left column

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Query Match          97.4%;    Score 1033.8;  DB 4;   Length 1762;
Best Local Similarity 98.4%;   Pred. No. 3.6e-303;
Matches 1044;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGACAACCATTATTTGATACTACTGA  60
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Db    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGACAACCATTATTTGATACTACTGA  60

Qy   61 CCCATTGGGTCTACAGTCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 120
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Db   61 CCCATTGGGTCTACAGTCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 120

Qy  121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
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Db  121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy  181 TGACAAATGCTACTGAATTAGTTCAGGACATTCAATAGGGAAAATATGCAACAACTCAT 240
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Db  181 TGACAAATGCTACTGAATTAGTTCAGGACATTCAATAGGGAAAATATGCAACAACTCAT 240

Qy  241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCCACT 300
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Qy  301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATGAGAAAGAAGCAGCGCTTTCAGCA 360
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Db  301 GTGATGTCTTTCAGTATGAGAATTGGGACCTCTTCATGAGAAAGAAGCAGCGCTTTCAGCA 360

Qy  361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCATTGTAGCATCCTCAG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GTTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCATTGTAGCATCCTCAG 420

Qy  421 GAACATTAGAATTCACAGCAGAGGATTCACATGGACAGTGTCAATAAACGGAAGAA 480
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Db  421 GAACATTGAATTCACAGCAGAGGATTCACATGGACAGTGTCAATAAACGGAAGAA 480

Qy  481 GTGGAGCCTGCAAAAGGGGATCAGCCGATCAGTTCTTTAGCCGACTGAATTGGCTAACAA 540
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Db  481 GTGATGTCTTTCAGTATGAGAATTGGCAACTTAGTTGCACCGCGGG 540

Qy  541 AATCTGGAAACTCTTACCCCACATTGAAATGCTAACAATAAAAATTTCGACA 600
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Db  541 AATCTGGAAACTCTTACCCCACATTGAAATGCTAACAATAAAAATTTCGACA 600

Qy  601 AACTATACATCTCGGGGGATTCATCACCCGAGCTCAAACCAACAGCAGAGAATTGTACA 660
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Db  601 AACTATACATCTCGGGGGATTCATCACCCGAGCTCAAACAAAGAGCAGCAAAATTGTACA 660

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Db  661 TCCAAGAATCAGGACGAGTAACAGTTCTTAGCCGATAATCCCTA 720

Qy  721 ATATCGGATCTAGAACCGTGGGTTAGGGGTCAATCAGGCAGTAGCATATACTGGACCA 780
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Qy  781 TTGTAAAACCTGGAGATATCCTAATGATAAAACAGTAATGCAACTTAGTTGCACCGCGGG 840
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Qy  841 GATATTTAAATTGAAAACAGGGAAAGCTTCGTAAATGAGATCAGATCAGACCCCATAGACA 900
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Db  841 GATATTTAAATTGAAAACAGGGAAAGCTTCGTAAATGAGATCAGATCAGACCCCATAGACA 900

Qy  901 TTTGTGTGTCTGAATGTATTACACCAAATGAAGCATCCCAACGACAAACCATTTCAA 960
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Db  901 TTTGTGTGTCTGAATGTATTACACCAAATGAAGCATCCCAACGACAAACCATTTCAA 960

Qy  961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAAACACTTTAAAGC 1020
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Right column

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Qy 1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
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Db 1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061
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RESULT 5
US-09-506-286B-7
; Sequence 7, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 1762
;   TYPE: DNA
;   ORGANISM: Equine influenza virus H3N8
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (30)..(1724)
US-09-506-286B-7
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Query Match          97.3%;    Score 1032.2;  DB 4;   Length 1762;
Best Local Similarity 98.3%;   Pred. No. 1.1e-302;
Matches 1043;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGACAACCATTATTTGATACTACTGA  60
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Db    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGACAACCATTATTTTGATACCACTGA  60

Qy   61 CCCATTGGGTCTACAGTCAGTAGCAAATGGAACATTGGTAAAAACAATAACAGCCACCATTATGTCTGG 120
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Db   61 CCCATTGGGTCTACAGTCAGTAGCAAATGGAACAACCACCAGTGCAACACAGCCACCATTATGTCTGG 120

Qy  121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
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Db  121 GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy  181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
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Db  181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240

Qy  241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCCACT 300
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Db  241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGACCCCCCACT 300

Qy  301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATGAGAAAGAAGCAGCGCTTTCAGCA 360
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Db  301 GTGATGTCTTTCAGTATGAGAATTGGGACCTCTTCATGAGAAAGAAGCAGCAGCGCTTTCAGCA 360

Qy  361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCATTGTAGCATCCTCAG 420
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Db  361 GTTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCATTGTAGCATCCTCAG 420

Qy  421 GAACATTAGAATTCACAGAGGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA 480
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Db  421 GAACATTGAATTCACAGAGGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA 480

Qy  481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540
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Qy  541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATTTCGACA 600
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Qy 421 GAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA 480
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Db 421 GAACATTGGAATTCACAGCAGAGGGATTCACATGGACAGTGTCACTCAAAACGGAAGA 480

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Db 481 GTGGATCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAG 540

Qy 541 AATCTGGAAACTCTTACCCACCAATTGAATGTGACAATGACATAAAAAATTTCGACA 600
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Db 541 AATCTGGAAACTCTTACCCACCAATTGAATGTGACAATGACATAAAAAATTTCGACA 600

Qy 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAAAGAGCAGACAGAATTGTACA 660
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Db 601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAAAGAGCAGACAGACAAAATTGTACA 660

Qy 661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGAGTCAACAAAACGATAGTCCCTA 720
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Db 661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGAGTCAACAAAACAATAATCCCTA 720

Qy 721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGGATAAGCATATACTGACCA 780
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Db 721 ACATCGGATCTAGACCGTGGGTTCAGGGGTCAATCAGGGATAAGCATATACTGACCA 780

Qy 781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
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Db 781 TTGTAAAACCTGGAGATATCCTAACGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840

Qy 841 GATATTTAAATTGAAAACAGGGAAAAGTCTGTAATGAAGCATCCCAAGCACACAAACCATTCAAA 900
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Db 841 GATATTTAAATTGAAAACAGGGAAAAGTCTGTAATGAAGCATCCCAAGCACACAAACCATTCAAA 900

Qy 901 TTTGTGTGTCTGAATGTATTACACCAAATTGAAGCATCCCCAACGACAAACCATTTCAAA 960
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Db 901 TTTGTGTGTCTGAATGTATTACACCAAATTGAAGCATCCCCAACGACAAACCATTTCAAA 960

Qy 961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020
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Db 961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy 1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
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Db 1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061

RESULT 4
US-10-434-811A-10
; Sequence 10, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-434-811A-10

Qy 961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020
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Db 961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy 1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
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Db 1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061

RESULT 3
US-10-065-133A-10
; Sequence 10, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-10-065-133A-10

Query Match   97.4%;   Score 1033.8; DB 4; Length 1762;
Best Local Similarity 98.4%;   Pred. No. 3.6e-303;
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60
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Db 1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60

Qy 61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACACACAGCCACATTATGTCTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGCAACACACAGCCACATTATGTCTGG 120

Qy 121 GACACCCATGCAGTAGCAAATGAACATTGGTAAAAACAATAACTGATGACCAAAATTGAGG 180
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Db 121 GACACCCATGCAGTAGCAAATGAACATTGGTAAAAACAATAACTGATGACCAAAATTGAGG 180

Qy 181 TGACAAATGCTACTGGAATTAGTTCAGAGCATTCAATAGGGAAAAATGCAACAACTCAT 240
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Db 181 TGACAAATGCTACTGGAATTAGTTCAGAGCATTCAATAGGGAAAAATATGCAACAACTCAT 240

Qy 241 ATAAGTTCTAGATGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGAAATTGAGG 300
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Db 241 ATAGAGTTCTAGATGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGAACCCCACT 300

Qy 301 GTGATGTCTTCCAGTATGCCAGTATGAGAATTGGGACCCTTCATAGAAGAGCAGCGCTTTCAGCA 360
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Db 301 GTGATGTCTTTCAGTATGCCAGTATGGGACCCTTCATAGAAGAGCAGCGCTTTCAGCA 360

Qy 361 ATTGCTACCCATGACATCCCTGACTATGCATCGCCTCCGGTCATTGTAGCATCCTCAG 420
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Db 361 GTTGCTACCCATGACATCCCTGACTATGCATCGCCTCCGGTCATTGTAGCATCCTCAG 420

; SEQ ID NO 10
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Equine influenza virus,H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1724)
; OTHER INFORMATION:
US-09-762-861B-10

Query Match   97.4%; Score 1033.8; DB 4; Length 1762;
Best Local Similarity   98.4%; Pred. No. 3.6e-303;
Matches 1044; Conservative   0; Mismatches 17; Indels   0; Gaps   0;

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Qy   61 CCCATTGGGTCTACAGTGCAAAACCCAACCAGTGAAACACACAGCCACATTATGTGTCTGG 120
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Db 121 GACACCATGAGTAGCAAATGGAACATTGGAACAACATTGGTAAAAACAATAACTGATGAGACCAAATTGAGG 180

Qy 181 TGACAAATGCTACTGAATTAGTTCAGAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
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Qy 241 ATAAAGTTCAGATGGAAGAAATTGCACATTAATAGATGCAAGTGCTAGGAGACCCCCACT 300
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Qy 301 GTGATGTCTTCAGTATGCAATGGGACCTCTTCATAGAAAGAGCAGCGCCTTTCAGCA 360
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Db 301 GTGATGTCTTCAGTATGCAATGGGACCTCTTCATAGAAAGAGCAGCGCCTTTCAGCA 360

Qy 361 ATTGCTACCCATATGACATCCCTGACTATGCATGCTCCGGTCCGGTCCATTGTAGCATCCTCAG 420
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Db 361 GTTGCTACCCATATGACATCCCTGACTATGCATGCTCCGGTCCGGTCCATTGTAGCATCCTCAG 420

Qy 421 GAACATTAGAATTCACAGCAGAGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA 480
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Db 421 GAACATTGGAATTCACAGCAGAGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA 480

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Db 481 GTGGATCCTGCAAAAGGGGAATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAG 540

Qy 541 AATCTGGAAACTCTTACCCCACCATTGGACAATGCCTAACAATAAAAATTCGACA 600
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Qy 601 AACTATACATCTGGGGGATTCATCACCCGAGTCAAACCAACAGCAGAACAGAATTGTACA 660
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Db 601 AACTATACATCTGGGGGATTCATCACCCGAGTCAAACCAACAGCAGAACAGAAATTGTACA 660

Qy 661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGTCAACAAACGATAGTCCCTA 720
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Db 661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGTCAACAAACGATAATCCCTA 720

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 ACATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGCGGATAAGCATATACTGGACCA 780

Qy 781 TTGTAAAACCTGAATTGTTGTCTGAATGTATTACACCGAAGTTGCACCGGGG 840
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Db 781 TTGTAAAACCTGAATTGTTGTCTGAATGTATTACACCGAAGTTGCACCGGGG 840

Qy 841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAAGATCAGATGAGACCCATAGACA 900
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Db 841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAAGATCAGATGAGACCCATAGACA 900

Qy 901 TTTGTGTGTCTGAATGTATTACACCGAAGCAATGGAAGCATCCCCAAGGACAACCATTTCAAA 960
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Qy 961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
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Qy 1021 TGGCCACTGGGATGGAGGAATATACCAGAAAAGCAAATCAGA 1061
          ||||||||||||||||||||||||||||||||||||||||||
Db 1021 TGGCCACTGGGATGGAGGAATATACCAGAAAAGCAAATCAGA 1061

RESULT 2
US-09-762-861B-10
; Sequence 10, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HK2-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1

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              GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      March  1, 2005, 03:20:06 ; Search time 219 Seconds
                                 (without alignments)
                                 7927.350 Million cell updates/sec

Title:           US-10-826-929A-1
Perfect score:   1061
Sequence:        1 agcaaaagcagggggatatt..........taccagaaaagcaaatcaga 1061

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:         2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database   :     Issued Patents NA:*
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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Match	Query Length	DB	ID			Description
1	1033.8	97.4	1762	4	US-09-506-286B-10	28	607.2	57.2	US-09-004-422-54	3	Sequence 10, Appl	Sequence 54, Appl
2	1033.8	97.4	1762	4	US-09-762-861B-10	29	607.2	57.2	US-09-918-568-54	4	Sequence 10, Appl	Sequence 54, Appl
3	1033.8	97.4	1762	4	US-10-065-133A-10	30	549.2	51.8	US-08-453-848-6	2	Sequence 10, Appl	Sequence 6, Appli
4	1033.8	97.4	1762	4	US-10-434-811A-10	31	549.2	51.8	US-09-169-027-6	2	Sequence 10, Appl	Sequence 6, Appli
5	1033.2	97.3	1762	4	US-09-506-286B-7	32	544.4	51.3	US-08-453-848-14	2	Sequence 7, Appli	Sequence 14, Appl
6	1032.2	97.3	1762	4	US-09-762-861B-7	33	544.4	51.3	US-09-169-027-14	3	Sequence 7, Appli	Sequence 14, Appl
7	1032.2	97.3	1762	4	US-10-065-133A-7	34	541.2	51.0	US-09-232-468A-21	4	Sequence 7, Appli	Sequence 21, Appl
8	1032.2	97.3	1762	4	US-10-434-811A-7	35	541.2	51.0	US-09-784-984B-17	4	Sequence 7, Appli	Sequence 17, Appl
9	1019.2	96.1	1698	4	US-09-622-951-1	36	541.2	51.0	US-08-453-848-20	2	Sequence 1, Appli	Sequence 20, Appl
10	1018.4	96.0	1762	1	US-08-105-483-300	37	541.2	51.0	US-09-169-027-20	3	Sequence 300, App	Sequence 20, Appl
11	1018.4	96.0	1762	1	US-08-709-209-300	38	148.2	14.0	US-08-105-483-279	1	Sequence 300, App	Sequence 279, App
12	1018.4	96.0	1762	1	US-08-458-101-300	39	148.2	14.0	US-08-709-209-279	1	Sequence 300, App	Sequence 279, App
13	1004.8	94.7	1695	4	US-09-506-286B-12	40	148.2	14.0	US-08-458-101-279	1	Sequence 12, Appl	Sequence 279, App
14	1004.8	94.7	1695	4	US-09-762-861B-12	41	127.2	12.0	US-08-686-968C-226	3	Sequence 12, Appl	Sequence 226, App
15	1004.8	94.7	1695	4	US-10-065-133A-12	42	122.4	11.5	US-08-229-781-57	1	Sequence 12, Appl	Sequence 57, Appl
16	1004.8	94.7	1695	4	US-10-434-811A-12	43	122.4	11.5	US-08-630-918-57	1	Sequence 12, Appl	Sequence 57, Appl
17	1003.2	94.6	1695	4	US-09-506-286B-9	44	122.4	11.5	US-09-004-422-57	3	Sequence 9, Appli	Sequence 57, Appl
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19	1003.2	94.6	1695	4	US-10-065-133A-9						Sequence 9, Appli	
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22	976.2	92.0	1762	1	US-08-709-209-284						Sequence 284, App	
23	976.2	92.0	1762	1	US-08-458-101-284						Sequence 284, App	
24	947.2	89.3	1698	3	US-09-232-478-15						Sequence 15, Appl	
25	947.2	89.3	1698	1	US-09-785-055-15						Sequence 15, Appl	
26	607.2	57.2	1777	1	US-08-229-781-54						Sequence 54, Appl	
27	607.2	57.2	1777	1	US-08-630-918-54						Sequence 54, Appl	

                              ALIGNMENTS

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RESULT 1
US-09-506-286B-10
;  Sequence 10, Application US/09506286B
;  Patent No. 6482414
;  GENERAL INFORMATION:
;    APPLICANT:  Dowling, Patricia W.
;    APPLICANT:  Youngner, Julius S.
;    APPLICANT:  The University of Pittsburgh, of the Commonwealth
;    TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;    FILE REFERENCE: EQ-1-C2
;    CURRENT APPLICATION NUMBER: US/09/506,286B
;    CURRENT FILING DATE:  2000-02-16
;    PRIOR APPLICATION NUMBER: 09/133,921
;    PRIOR APPLICATION FILING DATE: 1998-08-13
;    PRIOR APPLICATION NUMBER: PCT/US99/18583
;    PRIOR FILING DATE: 1999-08-12
;    NUMBER OF SEQ ID NOS: 108
;    SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 10
;  LENGTH: 1762
;  TYPE: DNA
;  ORGANISM: Equine influenza virus H3N8
;  FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (30)..(1724)
US-09-506-286B-10

  Query Match             97.4%;  Score 1033.8;  DB 4;  Length 1762;
  Best Local Similarity   98.4%;  Pred. No. 3.6e-303;
  Matches 1044;  Conservative  0;  Mismatches  17;  Indels  0;  Gaps  0;

Qy     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA 60
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Qy    61 CCCATTGGTCTCACAGTCAAAACCCACCAGTGGAAACAACAACAGCACAGCCACCATTATGTCTGG 120
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Db    61 CCCATTGGTCTCACAGTCAAAACCCACCAGTGGAAACAACAACAGCACAGCCACCATTATGTCTGG 120

Qy   121 GACACCATGCAGTAGCAGCAAATGGTAAAAACAATAACTGATGACCAAATTGAGG 180
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Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
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Qy   241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGCAATGCTAGGAGACCCCACT 300
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Db   241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCTAGGAGCAATGCTAGGAGACCCCACT 300
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Tue Mar 1 09:55:55 2005

us-10-826-929a-1.rng

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Db       ||| ||||| | ||||||||| |||     |  |||||||| | ||||||| ||||||  ||
     181 AGTTCCTCAACAGGTAGAATATGGACAGTCCTCACCGAATCCTTGATGGGAAAAAACTGC 240

Qy   267 ACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGG 326
         |||  ||||||| |||||| ||||||||||||||| ||||||||| ||||||| |||||
Db   241 ACACTGATAGATGCTCTATTGGGAGACCCTCATTGTGATGGCTTCAAAAATGAGAAATGG 300

Qy   327 GACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGAC 386
         |||||| |   || |||| ||  |  ||||| |||||||   |||||| ||| |||| |
Db   301 GACCTTTTGTTGAACGCAGCAAAGCTTTCAGCAACTGTTACCCTTATGATGTGCCAGAT 360

Qy   387 TATGCCATCGCTCCGGTCCATTGTGTAGCAATCCTCAGGAACATTAGAATTCAGCAGAGGA 446
         |||||| |   || || ||||| | || | ||||| |||   |||| ||||| |||||| |
Db   361 TATGCCCTCTTCTTAGGTCACTAGTTGCCTCGTCAGGAGTTTATCAATGAAGGC 420

Qy   447 TTCACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGATCAGCC 506
         |||| ||||||||| |||||| ||||||   |||| ||| |||||||||| |||||
Db   421 TTCAATTGGACTGGAGTCACTCAGAGTGGGGAAGCTATGCTTGCAAAAGGGGATCTGAT 480

Qy   507 GATAGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTG 566
         |||| ||||| |  ||| |||| ||| |||  |   ||||| | || |||  |||||
Db   481 AAAAGTTTCTTCAGTGACTGAATTGGTGTACGAATCAGAAAGCAAATATCCAGTGCTG 540

Qy   567 AATGTGACAATGCCTAACAATAAAAATTCGACAACTATACATCTCGGGGATTCATCAC 626
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Db   541 AACGTGACTATGCCAAACAATGGCAATTTTGACAAACTGTACATTTGGGGGTTCACCAC 600

Qy   627 CCGAGCTCAAACCAACACAGCAGAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTC 686
         |||||| ||||  |||| ||| ||| || || |||||| |   ||||||||| |||||||
Db   601 CCGAGCACCGGACAAAGAACAAACCAACCTATATGTTCGAGCATCAGGAGAGTCACAGTC 660

Qy   687 TGACAAAAGAGAGTCAACAAACAGTAGTCCCTAATATCGGATCGGGTCGTGGGTTAGG 746
         | || |  | |||||| |||  | || ||| || ||| ||||  |  ||||||| |||
Db   661 TCTACCAAGAGAAGCCAGCAAACTGTAATCCCGGAATATCGGGTCTAGACCCTGGGTAAGG 720

Qy   747 GGTCAATCAGGCAGGATAAGCAGTATACTGGACCATTGTAAAACCTGGAGATATCCTAATG 806
         ||| |  | | |||||| || ||| ||| |||| || || |||||| |||||| |||| |
Db   721 GGTCTGTCTAGTAGAATAAGTATCTATTGGACAATAGTAAAACCGGGACACATACTGTTA 780

Qy   807 ATAAACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAA 866
         ||  || |||| |||| || || || | |  || ||| |||||||||| ||||| ||||
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Qy   927 AATGGAAGCATCCCAACGACAAACACCATTTCAAAAATGTTACATCAAAGTTACATATGGAAAA 986
         |||||||| |||||||| | ||||| ||||||||||  ||  |||||| |||||| |||||
Db   901 AATGGAAGCATTCCCAATGACAACAAGCCCTTTCAAAACGTAAACAAGTAAACAACATATGGGGCA 960

Qy   987 TGCCCCAAGTATATCAGGCAAAACACTTTAAAGCTGGGCCACTGGAGGATGAGGAATATACCA 1046
         || |||||||| | |  ||||||  ||  ||| ||| | |||||| ||| |||||| ||||||
Db   961 TGTCCCAAGTATGTTAAGCAAAAACACTCTGAAGTTGGCAACAGGGATGCGGAATGTACCA 1020

Qy  1047 GAAAAGCAAATCAGA 1061
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Db  1021 GAGAAACAAACTAGA 1035
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Search completed: March 1, 2005, 03:44:48
Job time : 678 secs

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XX
DT   07-JAN-2003  (first entry)
XX
DE   Influenza A virus (A/Bangkok/1/79) haemagglutinin partial cDNA.
XX
KW   Influenza; Influenza A virus; pathogenicity; RNA viral disease;
KW   viral infection; selenium; vaccine; virucide; anti-HIV; gene; ss.
OS   Influenza A virus.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..1091
FT                  /tag= a
FT                  /partial
FT                  /product= "haemagglutinin protein"
XX
PN   WO200278717-A2.
XX
PD   10-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-EP003025.
XX
PR   28-MAR-2001; 2001US-00819387.
XX
PA   (NEST ) SOC PROD NESTLE SA.
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Beck M, German B, Levander O, Van Dael P;
XX
DR   WPI; 2002-759948/82.
DR   P-PSDB; ABP53895.
XX
PT   Treatment of influenza or reducing the risk of contracting influenza
PT   involves administering selenium to an individual.
XX
PS   Example 1; Page; 31pp; English.
XX
CC   The present invention describes a method for treating influenza or
CC   reducing the risk of contracting influenza, which involves administering
CC   selenium to an individual. Also described is a method for enhancing the
CC   efficacy of a viral vaccine by administering an antioxidant, preferably
CC   selenium, to an individual receiving the viral vaccine. The method can be
CC   used for treating influenza, for reducing the risk of contracting
CC   influenza, and for enhancing the efficacy of viral vaccine (preferably
CC   influenza vaccine) in an infant, elderly, a patient or a pet. It can also
CC   be used for treating virus such as coxsackie and HIV virus. The method
CC   provides an improved treatment for viral infection, by reducing in vivo
CC   mutations of the RNA virus. The method also improves a vaccine used to
CC   prevent transmission of an RNA viral disease. The present sequence
CC   encodes the haemagglutinin protein from Influenza A virus.
CC   (A/Bangkok/1/79). N.B. The present sequence is not given in the
CC   specification, but is taken from the Genbank accession number AF201843,
CC   as specified on page 7
XX
SQ   Sequence 1091 BP; 345 A; 227 C; 255 G; 264 T; 0 U; 0 Other;

Query Match             53.4%;  Score 566.2;  DB 6;  Length 1091;
Best Local Similarity   72.4%;  Pred No. 1.8e-149;
Matches  749;  Conservative   0;  Mismatches 283;  Indels   3;  Gaps   1;

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Db    1 ATGAAGACTATCATTGCTTTGAGCTACATTTTATGTCTGGTTTCGCTCAAACACTTCCC 60

Qy   90 --AGTGGAAACAACACAGCCACCATTATGTCTGGGACACACCATGGCAAAATGGAACA 146
          | |||||| |||| ||||||||| |||||||||||||||| || |||||||||||
Db   61 GGAAATGACAACAGCACAGCAACCGTGTCCTGGGACACCATGCCCAAACGGAACG 120
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Qy  118 TGGGACACCATGCCAGTAGCAGTGCAAATGGTAAAAACAATAACTGATGACCAAATTG 177
Db  121 TGGCACATCATGTGGCCAAACGGAACGCTAGTGAAAAACAATCACGAATGATCAGATTG 180
Qy  178 AGGTGACAAATGCTACTACTGAATTCAGAGCATTTCAATAGGGAAAATATGCAACACT 237
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Db  361 GCAACTGTTTACCCTTATGATGTGCCAGATTATGCCTCCCTTAGTGCACTAGTTGCCTCGT 420
Qy  418 CAGGAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAA 477
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Qy  478 GAAGTGAGGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTAGCCGACTGAATTGGCTAA 537
Db  481 GAAGCTATGCTTGCAAAAGGGGACCTGATAACAGTTTCTTCAGTGACTGAACTGGTTGT 540
Qy  538 CAAAAATCTGGAAACTCTTACCCCACATTGAAATGTGACAATGCCTAACAATAAAAATTCG 597
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Qy  598 ACAAACTATACATCTGGGGGATTCATCACCCAGCTCAAACCAACAGCAGAGAATTGT 657
Db  601 ACAAACTGTACATTTGGGGAGTTCACCACCCCGAGCTCAAACAAAGAACAAACCAAACTAT 660
Qy  658 ACATCCAAGAATCAGGAACGACGGAGTAACAGTCTCAACAAAAGAGAGTCAACAAACGATAGTCC 717
Db  661 ATGTTCAAGCATACCAGGGGAGTCCAGTCGTCCAAGAGAGCCAGCAAACTATAATCC 720
Qy  718 CTAATATCGGATCTAGACCGTGGGTGGGTTAGGGGTCAATCAGGGTCATAATACTGGA 777
Db  721 CGAATGTCGGGTCTAGACCCTGGGTAAGGGGTCTGTCTAGTAGAATAAGCATCTATTGGA 780
Qy  778 CCATTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATCAGTAATGGCAACTTAGTTGCCACGGC 837
Db  781 CAATAGTAAAACCCGGGAGACATACTGTTAATTAATAGCAACGGGAAACCCTTAATTGCTCCTC 840
Qy  838 GGGGATATTTTAAATTGAAAAACAGGGGAAAAGCTCTGTAAATGAGATCAGATGCGACCCCATAG 897
Db  841 GGGGTTACTTCAAAATACGCCACTGGGAAAAGCTCAATAATGAGTGCTCAGATGCACCCCATG 900
Qy  898 ACATTTGTGTCTGAATGTATTACACACCAAATGGAAGCATCCCCAAACGGACAAACCATTTC 957
Db  901 GCACCTGCAGTTCTGAATGCATCACTCCAAATGGAAGCATTCCCAAATGACAAGCCCCTTTC 960
Qy  958 AAAATGTGAACAAGTTACATATGGAAAATGCCCCAAGTATATCGGCAAAACACTCTTAA 1017
Db  961 AAAACGTAAACAGAATCACATATGGGGCATGTCCCAAGTATGTTAAGCAAAACACTCTGA 1020
Qy 1018 AGCTGGCCACTGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
Db 1021 AGTTGGCACAGGGGATGCCGAATGTACCAGAGAAACAACTAGA 1064
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Qy  147 TTGGTAAAACAATAACTGATGACCCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAG 206
Db  121 CTAGTGAAAAACAATCACGAATGATCAAATTGAAGTGACTAATGCTACTGAGCTGTTCAG 180
Qy  207 AGCATTTCAATAGGGAAAATATGCAACACTCATATAAAGTTCAACAACTGAAGAAATTGC 266
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RESULT 15
ABQ82724
ID   ABQ82724 standard; cDNA; 1091 BP.
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AC   ABQ82724;
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Db    721 CGAATATCGGGTCTAGACCCTGGGTAAGGGGTCTGTCTCGTAGTAGAATAAGCATCTATTGGA 780
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Qy    778 CCATTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGC 837
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Db    781 CAATAGTTAAACCGGGAGACATACTGTAATTAATAGTAATGGGAACCTAATTGCTCCTC 840

Qy    838 GGGGATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAG 897
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Db    841 GGGGTTATTTAAAATGCCACTCGGGAAAGCTCAATAATGAGGTCAGATGCACCTATTG 900

Qy    898 ACATTTGTGTGTCTGAATGTATTACCCAAATGAAGCATCCCCAACGACAAACCATTTC 957
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Db    901 GCACCTGCATTTCTGAATGCATCACTCCAAATGACAATCCCCAATGACAGCAGCCCTTTC 960

Qy    958 AAAATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGGCAAAACACTTAA 1017
              |||||| ||||| ||||| |||||||||||||  ||||||||||||| |||||||||||
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Db   1021 AGTTGGCAACAGGGGATGCGGAATGTACCAGAGAAACAAACTAGA 1064
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RESULT 14
AAN70642
ID    AAN70642 standard; cDNA; 1762 BP.
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AC    AAN70642;
XX
DT    27-AUG-2003  (revised)
DT    25-MAR-2003  (revised)
DT    29-APR-1991  (first entry)
XX
DE    Sequence encoding influenza HA protein.
XX
KW    HA; vaccine; ds.
XX
OS    Influenza A virus; 'A/Niigata 102181'.
XX
PN    JP62051992-A.
XX
PD    06-MAR-1987.
XX
PF    30-AUG-1985;  85JP-00192915.
XX
PR    30-AUG-1985;  85JP-00192915.
XX
PA    (KAGA ) KAGAKU KASEI RYOHO KENKYUSHO.
XX
DR    WPI; 1987-104909/15.
XX
PT    Recombinant plasmid - combines influenza virus gene and transformation
PT    enzyme and can be used for prepn. of influenza virus protein.
XX
PS    Disclosure; Fig 3; 14pp; Japanese.
XX
CC    Sequence may be inserted into a plasmid under the control of a
CC    phosphatase promoter, and used to transfor an E.coli expression system.
CC    The HA protein product may be used as vaccine against influenza viral
CC    infection. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-
CC    AUG-2003 to correct OS field.)
XX
SQ    Sequence 1762 BP; 579 A; 359 C; 404 G; 420 T; 0 U; 0 Other;
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Query Match           55.2%;  Score 585.6;  DB 1;  Length 1762;
Best Local Similarity  72.6%;  Pred. No. 7.1e-155;
Matches  772;  Conservative  0;  Mismatches  289;  Indels  3;  Gaps  1;

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Qy     61 CCCATTGGGTCTACAGTCAAAAC---CCAACCAGTGGAAACAACACAGCCACATTATGTC 117
             |||||||| ||||| |  ||||    ||| ||| |||||| |||||||||||| |||||||
Db     61 TCTGTCTGGTTCTCCGGCCCAAGACTTTCCAGGAAATGAAACAACAACAGCAGCCTGTGCC 120
```

[sequence alignment continues for RESULT 14 match, columns Qy and Db]

```
Query Match           56.4%;  Score 598.4;  DB 6;  Length 1764;
Best Local Similarity  73.3%;  Pred. No. 1.7e-158;
Matches  780;  Conservative  0;  Mismatches  281;  Indels  3;  Gaps  1;

Qy      1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGAGCAACCATTATTTGATACTACTGA 60
             |||||||||||||||||||||| ||| |||||||||||| |||| |||||||| |||||
Db      1 AGCAAAAGCAGGGGATAATTCTATTAACCATGAAGAAAACTATCATTGCTGTTTTGATACATT 60

Qy     61 CCCATTGGGTCTACAGTCAAAAC---CCAACCAGTGGAAACAACACAGCCACATTATGTC 117
             |||||||| | ||| |  ||||    ||| ||| |||||| |||||||||||| |||||||
Db     61 TCTGTCTGGTTCTCCGGCCCAAGACTTTCCAGGAAATGAAACAACAACAGCAGCCTGTGCC 120

Qy    118 TGGGACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTG 177
             |||||| || |||  |  ||||  |||||| |||   || || |  |||||| |||||| |
Db    121 TGGGACATCATGCGGTGCCAAACGGAACACTAGTGAAAACAACAGTGATCAGATTG 180

Qy    178 AGGTGACAAATGCTACTACTGGGTTCAGTGATTTCAATAGGAAAATATGCAACAACT 237
             ||||||| |||| |||| ||||| ||||| ||||||||||   ||||| |||||||||
Db    181 AAGTGACTAATGCTACTGAGCTGGTTCAGTGTTCCTCAACGGGAAAATATGCAACAATC 240

Qy    238 CATATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCACTGCTGGGGACCCCC 297
             |||||||||||||| || || |||| || ||||| |  ||| ||  || |||||| |||
Db    241 CTCATCGAATCCTTGATGAATAGACTGCACACTGATACTCTATTGGGGGACCCCTC 300

Qy    298 ACTGTGATGTCTTCCAGTATGAGAATTGGGACCCTCTTCATAGAAGAAGCAGCGGCTTTCA 357
             |||||||| || |||| || |||| |||||||||||| ||||||||||||| ||||||||||
Db    301 ATTGTGTGATGCTTTCAAAATGGGGACCCTTTCGTTGAACGCAGCAGCAAAGCTTTCA 360

Qy    358 GGAATTGCTACCCATCCTGACATCCCTGACTCGCTCCGGTCCCATTGTAGCGATCCT 417
             ||||| |||| ||||| |||| || ||||| | ||| ||||| |||| |||| |||||
Db    361 GCAACTGTTTACCCTTATGATGTGCCAGATTATGCCTCCCTCCCTAGTGTCACTAGTTGCTCTGT 420

Qy    418 CAGGAACATTAGAATTCACAGCAGCAGGATTCACATGACCACATGGTCACTCAAAACGGAA 477
             |||| ||||| || |||||| ||| ||| || ||| || ||   ||||||||| |||||
Db    421 CAGGCACCTCTGGAGTTTATCAGTGAAGGCTTCACTGGAACTGGGGTCACTCAGAATGGGG 480

Qy    478 GAAGTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGGAATTGGCTAA 537
             ||||| |||  | | |||||||  |||||||| ||||||||  | |||| ||| | |||
Db    481 GAAGCAATGCTGTTCAAAAGGGGACCTGATACGGGGTTTTTCAGTGAACTGGTTGT 540

Qy    538 CAAAATCTTCGAAACTCTTACCCCACCATTGAAATGTGACAATGCCCAAACAATAAAAATTCG 597
             |||||||||   |||| |||  ||| ||||||| ||| || || |||  |||| ||||  ||||
Db    541 ACAAATCAGGAAGACACATATCCAGTGCTGACGTGACTATGCCAAAACAATGACAATTTTG 600

Qy    598 ACAAACTATCATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGAATTGT 657
             |||||||||| |||||||| |||||| |||||  |||||||||||||| |||||||||
Db    601 ACAAACTATCACATTGGGGCGGTTCACCACCACCCGAGCACCCGAGCACCAAGAGAAGCCAGCCTAT 660

Qy    658 ACATCCAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGTCC 717
             ||||||| |||||| |  || | ||  |||  || || || ||||||||| |||||||
Db    661 ATGTTCAAGCACAGGGAGAGTCACAGTTCAACGTCTCTACCAAGAGAAGCCAGCAAACTATAATCC 720

Qy    718 CTAATATCGGATCTAGACCCTGGGTAGGGTTAGGGTCAATCAGGCAGGCATATACTGGA 777
             ||||| ||  ||||| |||  |||  |  |||||| ||||| || |||| ||| ||||||
Db    721 CCCATTGGGTCTACAGTCAAAAC---CCAACCAGTGGAAACAACACAGCCACATTATGTC 117
```

PR   23-JUN-2000; 2000US-0213650P.
XX
PA   (AMCY) AMERICAN CYANAMID CO.
XX
PI   Galarza JM, Latham TE;
XX
DR   WPI; 2002-139923/18.
DR   P-PSDB; ABB05767.
XX
PT   Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
PT   polypeptide, useful in diagnosis and for generating new influenza A
PT   variant strains.
XX
PS   Claim 1; Page 61-64; 103pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) having the
CC   complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
CC   strand, antigenomic message sense. ABA93934 to ABA93944 encode the
CC   Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774
CC   from the present invention. (I) is useful for designing polymerase chain
CC   reaction (PCR) primers for use in a PCR assay to detect the presence of
CC   the corresponding virus segment in a sample or for designing and
CC   selecting peptides for use in an enzyme linked immunosorbant assay to
CC   detect the presence of the corresponding protein produced by that segment
CC   in a sample; hence is useful in diagnosis and may be modified by mutation
CC   to generate new influenza A variant strains. ABA94945 to ABA94039
CC   represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
CC   are used in an example from the present invention
XX
SQ   Sequence 1765 BP; 568 A; 355 C; 414 G; 428 T; 0 U; 0 Other;

Query Match   56.7%; Score 601.6; DB 6; Length 1765;
Best Local Similarity   73.5%; Pred. No. 2.1e-159;
Matches 782; Conservative   0; Mismatches 279; Indels   3; Gaps   1;

Qy   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACACCATTATTTTGATACTACTGA 60
           |||||||||||||||||||||| || |||||||| |||||| ||| ||||| |||
Db   1 AGCAAAAGCAGGGGATAATTCTATTAACCATGAAGACTATCATTGCTTTGAGCTACATTT 60

Qy   61 CCCATTGGGTCTACAGTCAAAAC--CCAACCAGTGAAACAACACAGCCACATTATGTC 117
           | ||||| || ||| ||||| ||||||||||| |||||| ||| |||| |||||
Db   61 TCTGTTCTGGTTCTCCGGCCAAAACTTTCCAGGAAATGACCAACGACCACAACGCTGTGCC 120

Qy   118 TGGGACACCATGCAGTAGCAAATGGACATTGGTAAAAACAATAACTGATGACCAAATTG 177
           |||||||| ||| | |||| ||||| ||||| |||||||| ||| ||||||||| |||
Db   121 TGGGACATCATGCGGGTGCCAAACGGAACACTAGTGAAAACAATCACAAATGATCAGATTG 180

Qy   178 AGTGACAAATGCTACTGAATTAGTTCAGAGCATTCAATAGGGAAAATATGCCAACAACT 237
           |||| |||||||||| ||| |||||| ||| | ||||||||||| || |||||||||||
Db   181 AAGTGACTAATGCTACTGAGCTGGTTCAGAGTTCCAACGGGAAAAATATGCCAACAATC 240

Qy   238 CATATAAAGTTCTAGATGGAAGAAATTGCACATTAATGATGCTAGGAGACCCCC 297
           || || ||||| || | |||||||||| ||||||| |||||| ||||| ||||||
Db   241 CTCATCGGAATCCTTGATGGAATAGACTGCACACTGATGATGCTCTATTGGGGGACCCTC 300

Qy   298 ACTGTGATGTCTTCCAGTATGAGAATTGGGACACCTCTTCATAGAAAGAAGCAGCGCTTTCA 357
           || |||| | ||||||| |||| || || |||||| || |||| | ||||| |||||| |||
Db   301 ATTGTGATGGCTTCCAAAATGAGACGATGGGGACCTTCGTTGAACGCAGCAGCAAAGCTTTCA 360

Qy   358 GCAATGCTACCCATATGACATCCCTGACTATGCCATCGTCCGGTCCATTGTAGCATCCT 417
           |||||| || | |||| |||| | |||| ||| |||| ||| |||||| ||| |||||
Db   361 GCAACTGTTACCCTTATGTGCCAGATTATGCCTCCCTTAGGTCTCACTAGTTGCCTCGT 420

Qy   418 CAGGAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAA 477
           |||| || || | ||||| |||||| || | ||| ||||||||| ||| ||||| ||||
Db   421 CAGGCACTCTGGAGTTTATCAGTGAAGGCTTCACTTGGACTGGGGTCCACTCAGAATGGGG 480

Qy   478 GAAGTGGAGCCTGCAAAAGGGGATCACGCCGAGTTTCTTTAGCCGACTGAATTGGCTAA 537
           || || || || |||||| | || ||| |||| |||| ||| ||| ||||| ||| ||
Db   481 GAAGCAATGCTTCAAAAAGGGGACCTGATAGCCGGTTTTTCAGTGACTAGACTGAACTGGTTGT 540

Qy   538 CAAAATCTGGAAACTCTTACCCCACAATTGAATGTGACAATGCCTAACAATAAAAATTCG 597
           ||||| || || || |||| ||||| ||||| |||||| |||| ||||||||||| | ||||||

Db   372 CTGTTACCCTTATGATGTGCCAGATTATGCTCCCTTAGTCACTAGTTGCCTCGTCAGG 431
Qy   422 AACATTAGAATTCACAGCAGGATTCACATGGACAGGTGTCACTCAAAACGAAGAAG 481
          |||| |||||||||||| ||| ||||||||||| ||||||||||||
Db   432 CACTCTGGAGTTTATCACTTGAGGGTTCACTTGGACTGGGTCACTCAGAATGGGGGAAG 491

Qy   482 TGGAGCCTGCAAAAGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAAA 541
          |||| ||||||||||| ||| |||||| ||| ||||||||||||||| |||||||
Db   492 CAATGCTTGCAAAAGGGGACCTGGTAGCCGTTTTTTCAGTAGACTGAACTGGTTGACCAA 551

Qy   542 ATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATTTGCACAA 601
          ||| ||||| ||||||| |||||| | |||||| |||||| ||||| || |||| ||
Db   552 ATCAGGAAGCACATATCCAGTGCTGACACGTGACTATGCCAAACAATGACAATTTGACAA 611

Qy   602 ACTATACACATCTGGGGAGTTCATCACCCGAGCTCAAACCAGACAGCACAGAATTGTACAT 661
          ||||||||||| ||| |||||||| || ||| |||||| ||| ||| |||||||
Db   612 ACTATACATTTGGGGGATTCACCACCCGAGCTCAAACCAGACCACGGAACCAGCCTGTATGT 671

Qy   662 CCAAGAATCAGGACGAGCTAACAGTCTCAACAAGAAGAAGTCAACAAACGATAGTCCCTAA 721
          |||| ||||||||| |||||| ||||||||||||| || ||||| | || | |||| ||
Db   672 TCAAGCATCAGGGAGAGTCACAGTCTTCTACCAGGGCCAATCAGGAAGCATCTATTGGACAAT 731

Qy   722 TATCGGATCTAGACCGTGGGTTAGGGTCTAAGGGTCTCTAGTAGAATAAGCATCTATTGGACAT 781
          |||||| ||| ||||| ||| ||||||| || ||||| | |||||| ||||||||||||||
Db   732 TATCGGGTCCAGACCCTGGGTAAGGGTCTAAGGGTCTGTCTAGTAGAATAAGCATCTATTGGACAAT 791

Qy   782 TGTAAAACGTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGGGG 841
          ||||||| ||| ||| | | ||||| ||| || ||| |||| || || | | |||
Db   792 AGTTAAGCCCGGACGTACTGGTAATTAATAGTAGTAATGGGAACCTTAATCGCTCCTCTGGGG 851

Qy   842 ATATTTTAAATTGAAAACAGGGAAAAGCCTGTAATGAGATCAGATGCCACCCATAGACAT 901
          | |||| |||| |||| ||||| ||| || || ||| || ||| | | | ||| |
Db   852 TTATTTCAAAATGCGCACTGGAAAAGTCAATAATGAGGTCAATGATGATGATCTATTGATAC 911

Qy   902 TTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCAAACCAAACCATTCAAAA 961
          |||| | || ||| || | ||||||||| |||||| ||| || | ||||| |||||
Db   912 CTGTATTTCTGAATGCATCACTCCAAATGAAGCATTCCCAATGACAAGCCCTTTCAAAA 971

Qy   962 TGTGAACAAGTTACATGCAGAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGCT 1021
          |||||||| | | ||| ||| ||||||||||||| | |||| || | |||||| ||
Db   972 CGTAAACAAGATCACATATGGAGCATGCCCCAAGTATGTGTTAAGCAAAACACCCTGAAGTT 1031

Qy 1022 GGCCACTGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
          ||||| ||| || | ||||| ||||| ||||| ||||
Db 1032 GGCAACAGGGATGCCGGAATGTACCAGGAGAAACAAACTAGA 1071

RESULT 12
ABA93937
ID   ABA93937 standard; DNA; 1765 BP.
XX
AC   ABA93937;
XX
DT   07-MAY-2002 (first entry)
XX
DE   Influenza A/Udorn/72 (H3N2) Strain HA encoding DNA SEQ ID NO:7.
XX
KW   Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
KW   Influenza A virus; genome; gene; ds.
XX
OS   Influenzavirus A.
XX
FH   Key   Location/Qualifiers
FT   CDS   30..1730
FT   /tag= a
FT   /product= "HA protein"
XX
PN   WO20020884-A2.
XX
PD   03-JAN-2002.
XX
PF   21-JUN-2001; 2001WO-US019826.
XX

FT   misc_feature   904..1734
FT   /tag= e
FT   /product= "stem region of C-terminal domain"
XX
PN   EP621339-A2.
XX
PD   26-OCT-1994.
XX
PF   94EP-00302819.
XX
PR   20-APR-1993; 93JP-00115216.
PR   16-MAR-1994; 94JP-00070194.
XX
PA   (TAKI) TAKARA SHUZO CO LTD.
XX
PI   Okuno Y, Isegawa Y, Sasao F, Ueda S;
XX
DR   WPI; 1994-325949/41.
DR   P-PSDB; AAH63390.
XX
PT   Human influenza-A virus haemagglutinin polypeptide(s) - useful in
PT   influenza-A vaccine composition.
XX
PS   Example 2; Page 54-58; 68pp; English.
XX
CC   This sequence was amplified using the primer sequences given in AAQ72852-
CC   54 and represents a cDNA which encodes the full length hemagglutinin (HA)
CC   gene of the H3N2 subtype of human influenza A virus, strain
CC   A2/Aichi/2/68. The full length protein encoded by this amplified cDNA
CC   contains two conserved regions, the A' region, TGMRN and the B region,
CC   QINGKLNR(L/V)IEK. These regions are close to each other in the stem of the
CC   HA molecule and they represent epitopes which are recognised by the
CC   antibody C179. C179 binds to the stem region of the HA molecule and thus
CC   inhibits the membrane fusion action of the HA molecule and neutralises
CC   the virus. Polypeptide molecules which contain the conserved peptide
CC   regions, A and B, esp. HA molecules lacking the globular head region (see
CC   also AAQ72807), are antigenically equivalent to the stem region of the HA
CC   molecule of influenza A virus. These artificial peptides may be used as
CC   vaccines for prophylaxis of influenza A virus infection. (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 1777 BP; 565 A; 363 C; 420 G; 429 T; 0 U; 0 Other;

Query Match   57.2%; Score 607.2; DB 2; Length 1777;
Best Local Similarity   74.0%; Pred. No. 5.6e-161;
Matches 784; Conservative   0; Mismatches 273; Indels   3; Gaps   1;

Qy   5 AAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGTATACTACTGACCCA 64
          ||||||||||||| ||| | ||||||||||||| ||||| ||| |||| |||||
Db   12 AAAGCAGGGGATAATTCTATTAATCATGAAGACCATTGCTTTGAGCTATATTTTCTG 71

Qy   65 TTGGGTCTACAGTCAAAAC---CCAACCAGTGGAAACAACACAGCCACATTATGTGTCTGGGG 121
          | ||||| | ||||| |||||| ||||| ||||||||||||| |||||||||||
Db   72 TCTCGGCTCTCCGGCCAAGACCTTCCAGGAAATGACAACAGCCAACGCGTGTGCCTGGGG 131

Qy   122 ACACCATGCAGTAGCAGTGAAATGGAACATTGGTAAAAACAATAACAATAACTGATGAGGT 181
          || |||||| ||| ||| || || ||| || || || |||||| |||| | |||| |||||
Db   132 ACATCATGCGGTGCCAAAGGAACTAGTGAAAACAATCACAGAATGATCAGATTGAAGT 191

Qy   182 GACAAATGCTACTGATTAGTTCAGAGCATTTCAGAGCTTCAGAGTTCAACAACAACTCATA 241
          ||| |||||||||||| | ||||||||||||||||||||||||||||||||||||||| ||
Db   192 GACTAATGCTACTGAGCTAGTTCAGAGCATTTCAGAGCTTCAGAGTTCAACAACAACTCCTCA 251

Qy   242 TAAAGTTCTAGATGGAAGAAATTGCACATTGACATGCAATGCATCAGGACAACCCCCACTG 301
          ||||||||||||| |||| ||||||| | ||| || |||||||| ||||||||||||
Db   252 TCGAATCCTTGATGAGAATAGAGCTCACACTGATGAGATGCTCTATTGGGAGGACCCTCATTG 311

Qy   302 TGATGTCTTCCAGTAGCAGTAGGATTGGGACCTTCTTCATAGAAAGAAGCAGCGCTTTCAGCAA 361
          | ||||| ||||||| |||| ||||| ||||| ||| || ||||||||| || |||||
Db   312 TGATGTTTTTCAAAATGAGACAGGGACCTTTCGGTTCGAACCGGTCAGCAGGAAGCTTTCAGCAA 371

Qy   362 TTGCTACCCATGACATCCCTGACTATGCGTCAATGCGCTTCCGGGTCTTGTAGCCATCCTCAGG 421
          || | | || | | ||| ||| || | |||||| || ||| |||

```
FT   CDS          1..1698
FT                /*tag= a
FT                /product= "haemagglutinin protein"
XX
PN   FR275l226-A1.
XX
PD   23-JAN-1998.
XX
PF   19-JUL-1996;    96FR-00009400.
XX
PR   19-JUL-1996;    96FR-00009400.
XX
PA   (INMR ) RHONE MERIEUX SA.
XX
PI   Audonnet JCP,  Bouchardon A,  Riviere MEA;
XX
DR   WPI; 1998-112826/11.
DR   P-PSDB; AAW44946.
XX
PT   Multi-valent polynucleotide vaccines against equine pathogens - consist
PT   of at least 3 plasmids able to express protective antigens from specified
PT   viruses.
XX
PS   Example 14; Fig 8; 49pp; French.
XX
CC   The invention relates to a multivalent vaccine for protecting horses
CC   against several pathogens, especially pathogens associated with
CC   respiratory and digestive diseases. The pathogens are especially selected
CC   from equine herpesvirus (EHV), equine influenza virus (EIV), Clostridium
CC   tetani, Borrelia burgdorferi, Eastern, Western or Venezuelan equine
CC   encephalomyelitis viruses (EEEV, WEEV and VEEV, respectively) and rabies
CC   virus. The vaccines are preferably composed of polynucleotide sequences
CC   encoding 3 antigens, all as part of vectors. This sequence represents the
CC   coding region of the EIV Fontainebleau strain haemagglutinin gene. The
CC   sequence was subcloned into the plasmid pVR1012 to generate plasmid
CC   pAB099 for use in the vaccine
XX
SQ   Sequence 1698 BP;  604 A;  319 C;  384 G;  391 T;  0 U;  0 Other;

Query Match        89.3%;   Score 947.2;   DB 2;   Length 1698;
Best Local Similarity  94.9%;   Pred. No. 3.8e-257;
Matches  979;  Conservative  0;  Mismatches  53;  Indels  0;  Gaps  0;

Qy         30 ATGAAGACAACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC  89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAGACAACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC  60

Qy         90 AGTGGAAACAACAACAGCCACATTATGTCTGGGACACCACCATGCAGTCAGTAGCAAATGGAACATTG 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTGGCAACAACAACAGCCACACTTATGTCTGGGACACCACCATGCAGTCAGTAGCAAATGGAACATTG 120

Qy        150 GTAAAAACAATAACTGATGACGAGAATTGAGGTGACAAATGCTACTGAGATTAGTTCAGAGC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAAAAACAATAACTGACGACGAGAATTGAGGTGACAAATGCTACTGAGATTAGTTCAGAGC 180

Qy        210 ATTTCAATAGGGAAAAATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTTCAATAGGGAAAAATGCAACACCATAGGGTTCTAGATGGAAGAAACTGCACA 240

Qy        270 TTAATAGATGCAATGCTAGGAGAATCTTCAGTGATGTCTTCCAGTATGAGAATTGGGAC 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTAATAGATGCAATGCTAGGAGAATCCCACTGTGATGTCTTTCAGTATGAGAATTGGGAC 300

Qy        330 CTCTTCATAGAAAGAGAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTTCATAGAAAGAAGAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 360

Qy        390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCATCGCTCCGGTCATTGTGGCATCTTCAGGAACATTAGAATTCACAGCAGAGGGATTC 420

Qy        450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGCGCCTGCAGAAGGGGATCAGCCGAT 509
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
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Db        421 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGCGCCTGCAGAAGGGGATCAGCCGAT 480

Qy        510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTCGGAAACTTCTACCCCACATTGAAT 569
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTTTTCTTTAGCCGACTGAATTGGCTAACAGAATTCTACCCCACATTGAAT 540

Qy        570 GTGACAATGCCTAACATTAGAAAATTCGACAACTATACATCTGGGGATTCATCACCCG 629
              ||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        541 GTAACAATGCCTAACAATTCGATAAACATTTCGATAAACATAACATCTGGGGATCCATCACCCG 600

Qy        630 AGTCAAACCAACAGCAGCAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCCAACAAACAATGAGCAGCAGCAAAATTGTATGTCCAAGAATTAGGACGAGTAACAGTCTCA 660

Qy        690 ACAAAAGAGTCAACAACGATAGTCCCTAATATGGATCTAGACCGTGGGTTAGGGGT 749
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAAAAGAGTCAACAACAACAATAATCCCCACATCGGATATCTAGACCGGGGGGTCAGGGGT 720

Qy        750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
              ||||||||||||||||||||||||||| |||| |||||||||||||||||||||||
Db        721 CAATCAGGCAGGATAAGCATATATGGACCATTGTGAAACCTGGAGATATCCTAATGATA 780

Qy        810 AACAGTAATGGCAACTTAGTTGCACCGGCGGGGGATATTTTAAATTGAAAACAGGGAAAAGC 869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAGTAATGGCAACTTAGTTGCACCGGCGGGGGATATTTTCAAAATGCGAACAGAAAAAAGC 840

Qy        870 TCTGTGAATGATCAGATGCACCCATAGACATTTGTGTGTCGAATGATTATTACCACAAAT 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTATAATGAGATCAGATGCACCCATAGACACTTGTGTGTCCGAGTGTATTATTACCACAAAT 900

Qy        930 GGAAGCATCCCCAACGACAAACCATTCAAAAATGGAACAAAGTTACATATGGAAAATGC 989
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGAAGCATCCCCACCGACACAAACCATTTCAAAATGGAACAAAGTTACATATGGAAAAATGC 960

Qy        990 CCCAAGTATATCAGGCAAAAACACTTTAAAGCTGCCACTGGGATGAGAATATACCAGAA 1049
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCCAAGTATATCAAGCAGAATACTTTGAGCGTCGGCCACTGGGATGAGGAATGTACCAGAA 1020

Qy       1050 AAGCAAATCAGA 1061
              ||||||||||||
Db       1021 AAGCAAATCAGA 1032
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RESULT 11
AAQ72855
ID   AAQ72855 standard; cDNA; 1777 BP.
XX
AC   AAQ72855;
XX
DT   25-MAR-2003  (revised)
DT   23-JUN-1995  (first entry)
XX
DE   Full length H3N2 influenza A virus, strain A2/Aichi/2/68 HA gene.
XX
KW   Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2; PCR;
KW   subtype; human; influenza A virus; immunogenic artificial peptide;
KW   antigen; vaccine; infection; polymerase chain reaction; primer; amplify;
KW   C179; region A; region B; ds.
XX
OS   Influenza A virus.
XX
FH   Key            Location/Qualifiers
FH
FT   CDS            36..1737
FT                  /*tag= a
FT                  /product= "Full length HA from H3N2 subtype"
FT   sig_peptide    37..84
FT                  /*tag= b
FT   misc_feature   85..246
FT                  /*tag= c
FT                  /product= "Stem region of N-terminal domain"
FT   misc_feature   247..903
FT                  /*tag= d
FT                  /product= "Globular head domain"
```

```
Qy    301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGATGTTTTCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCA 360

Qy    361 ATTGCTACCCATATGACATCCTGACTATGCATCGATCGGTCCGGTCCATTGTAGCATCCTCAG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTGGTACCCATATGACATCCTGACTATGCATCGATCGCTCCGGTCTATTGTGGCATCTTCAG 420

Qy    421 GAACATTAGAATTCACAGCAGAGGATTCACATGACAGGTGTCACTCAAAACGGAAGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GAACATTAGAATTCACAGCAGAGGATTCACATGACAGGTGTCACTCAAAACGGAAGAA 480

Qy    481 GTGGAGCCTGCAAAAGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTGGGGCCTGCAGAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAG 540

Qy    541 AATCTGGAACTCTTACCCCACCATTGAAATGTGACAATGCCTAACAATAAAAATTTCGACA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AATCTGGAAATTCTTACCCCACCATTGAATGTGACAATGCCTAACAATAACAATTTCGATA 600

Qy    601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAACAGCAGCAAAATTGTACA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACTATACATCTGGGGGATTCATCACCCGAGCACAACAATGAGCAGGACAAAATTGTATG 660

Qy    661 TCCAAGAATCAGGACCAGTAACAGTTCAACAAAAGAGAGTCAACAAACGATAGTGCCCTA 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TCCAAGAATTAGGGCCAGTAACAGTCTCAGGGGTCAACCAAACACAACAATAATCCCCA 720

Qy    721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGCGAGATAAGCATATACTGACCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACATCCGATCTAGACCGGGGGTCAGGGGTCAATCAGCGAGATAAGCATATATTGGACCA 780

Qy    781 TTGTAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTGTGAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840

Qy    841 GATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAATCAGATGCACCCATAGACA 900
          |||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||
Db    841 GATATTTCAAAATGCCAACAGAGGAAAAGCTCTATATGAGATCAGATGCACCCATAGACA 900

Qy    901 TTTGTGTGTCTGAATGTATTACACCAAGAAGCATCCCAACGACAACAACCCATTTCAAA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTTGTGTGTCCGAGTGTATTACACCAAGAAGCATCCCCAACGACAACAACCCATTTCAAA 960

Qy    961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACTTTAAAGC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAAGCAGAATACTTTGAAGC 1020

Qy   1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
          |||||||||||||||||||||||||||||||||||||||||
Db   1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061
```

RESULT 10
AAV49391
ID   AAV49391 standard; DNA; 1698 BP.
XX
AC   AAV49391;
XX
DT   28-OCT-1998 (first entry)
XX
DE   EIV Fontainebleau strain haemagglutinin gene.
XX
KW   Multivalent vaccine; horse; pathogen; respiratory disease; EHV; EIV;
KW   Clostridium tetani; Borrelia burgdorferi; equine influenza virus; VEEV;
KW   Eastern equine encephalomyelitis virus; equine herpesvirus; WEEV;
KW   Western equine encephalomyelitis virus; digestive disease; rabies virus;
KW   Venezuelan equine encephalomyelitis virus; vector; primer; PCR;
KW   amplification; haemagglutinin; ss.
XX
OS   Equine influenza virus.
XX
FH   Key   Location/Qualifiers

DE   EIV HA (A1/Fontainebleau/79).
XX
KW   Equine influenza virus; EIV; hemagglutinin; HA; A1/Fontainbleau/79;
KW   expression cassette; NYVAC; ALVAC; recombinant vector;
KW   polymerase chain reaction; PCR; vaccinia virus; H6 promoter;
KW   canarypox virus; Copenhagen vaccine strain; virulence factor;
KW   deletion loci; recipient loci; ss.
XX
OS   Synthetic.
XX
PN   WO9215672-A1.
XX
PD   17-SEP-1992.
XX
PF   09-MAR-1992;   92WO-US001906.
XX
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   06-MAR-1992;   92US-00847951.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E,   Perkus ME,   Taylor J,   Tartaglia J,   Norton EK;
PI   Riviere M,   De Taisne C,   Limbach KJ,   Johnson GP,   Pincus SE,   Cox WI;
PI   Francis J,   Gettig RR;
XX
DR   WPI; 1992-331718/40.
XX
PT   Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating
PT   against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,
PT   mumps etc.
XX
PS   Disclosure; Fig 24; 456pp; English.
XX
CC   The sequence given encodes the equine influenza virus (EIV) hemagglutinin
CC   (HA) (A1/Fontainbleau/79). This sequence was used to generate an
CC   expression cassette for the insertion of the EIV HA gene into NYVAC and
CC   ALVAC recombinant vectors. The HA gene sequence was isolated from an EIV
CC   cDNA library and then reconstituted aligned with the vaccinia
CC   sequence was fragmented and then reconstituted aligned with the vaccinia
CC   virus H6 promoter. NYVAC is derived from a Copenhagen vaccine strain of
CC   vaccinia virus and ALVAC is derived from a canarypox virus which has been
CC   modified by deletion of non-essential regions of the genome encoding
CC   known or potential virulence factors. The deletion loci of both vectors
CC   were engineered as recipient loci for the insertion of foreign genes. See
CC   also AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 1762 BP; 626 A; 331 C; 395 G; 410 T; 0 U; 0 Other;

Query Match   92.0%; Score 976.2; DB 2; Length 1762;
Best Local Similarity   95.0%; Pred. No. 2.4e-265;
Matches 1008; Conservative   0; Mismatches   53; Indels   0; Gaps   0;

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Qy      1 AGCAAAAGCAGGGGATATTTCTGTCAATCAATGAAGACAACCATTATTTTGATACTACTGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGCAAAAGCAGGGGATATTTCTGTCAATCAATGAAGACAACCATTATTTTGATACTACTGA 60

Qy     61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACAGCACCACTATTGTCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGCAACAACAGCACCACTATGTCTGG 120

Qy    121 GACACCCATGCAGTAGCAGTGAAATTGGTAAAAACAATAACTGGTACGACCAAATTGAGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GACACCCATGCAGTAGCAGTGAAATGGCAAATGGTAAAAACAATAACTGGTACGACCAAATTGAGG 180

Qy    181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAAATATGCAACAACTCAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGACAAATGCTACTGAATTAGTTCAGAGCACTTCAATAGGGAAAAATATGCAACACCCAT 240

Qy    241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCAATGGATGACCCCACT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATAGGGTTCTAGATGGAAGAAATGCACATTAATAGATGCAATGCAATGCTAGGAGGATCCCCACT 300
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Db      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    121 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 180

Qy  210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGGAAGAAATTGCACA 269
        ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  181 ATTTCAATAGGGAAAATATGCAACAACTCATATAGAGGGTTCTAGATGGGAAGAAATTGCACA 240

Qy  270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
        |||||||||||||||||||||||||||||         ||||||||||||||||||||||
Db  241 TTAATAGATGCAATGCTAGGAGACCCCCCATTGTGATGATTTCAGTATGAGAATTGGGAC 300

Qy  330 CTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCAATTGCTACCCATAGACATCCTGACTAT 389
        |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  301 CTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCAATTGCTACCCATAGACATCCCTGACTAT 360

Qy  390 GCATCGCTCCGGTCCATTGTAGCATCTCCAGGACATCATTAGAATTCACAGCAGAGGATTC 449
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  361 GCATCGCTCCGGTCCATTGTAGCATCTCCAGGACATCATTAGAATTCACAGCAGAGGGGTTC 420

Qy  450 ACATGGACAGGTGTCACTCAAAACGGAGAAGAAGTGGAGCTGCAAAAGGGGATCAGCCGAT 509
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 ACATGGACAGGTGTCACTCAAAACGGAGAAGAAGTGGAGCTGCAAAAGGGGATCAGCCGAT 480

Qy  510 AGTTTCTTTAGCCGACTGGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
        |||||||||||||||||||||||||||||||||||||||| ||||||||| ||||||||
Db  481 AGTTTCTTTAGCCGACTGGAATTGGCTAACAAAATCTGGAAATTCTTACCCCATATTGAAT 540

Qy  570 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTCGGGGATTCATCACCCG 629
        |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  541 GTGACAATGCCTAACAATAAAAATTTCGATAAACTATACATCTCGGGGATTCATCACCCG 600

Qy  630 AGCTCAAACCAACAGCAGCAGAATTGTACATCCAAGATCAGAGCGAGTAACAGTCTCA 689
        ||||||||| ||| ||| |||||||| ||||||||||||||||||||||||||||||
Db  601 AGCTCAAACAAAGAGCAGACAAAATTATATATCCAAGATCAGAGCGAGTAACAGTCTCA 660

Qy  690 ACAAAAAGAAGTCAACAACGATAGTGTCCCTAATATGCATTGTGTGTCTGGGTAGGGGT 749
        ||| ||||||||||||||| |||| || |||| |||| |||| ||||| |||||||||
Db  661 ACAGAAAGAAGTCAACAACAGTAATCCTACAATCCCTAACATGGCATCTAGGCCGTCAGGGGT 720

Qy  750 CAATCAGGCAGGATAAGCATATACTGGAACCATTGTAAACCTGAGATATCCTAATGATA 809
        |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db  721 CAATCAGGCAGGATAAGCATATACTGGAACCATTGTAAACCTGAGATATTCTAATGATA 780

Qy  810 AACAGTAATGGCAACTTAGTTGCACCGGGGATATTTAAATTGAAAACAGGGAAAAAGC 869
        ||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||
Db  781 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAATTGAGAACAGGGAAAAGC 840

Qy  870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTACCAAAT 929
        |||||||||||||||||||||| |||||||| ||||||||||||||||||||| |||||
Db  841 TCTGTAATGAGATCAGATGCACTCATAGACACTTGTGTGTCTGAATGTATTACACCAAAT 900

Qy  930 GGAAGCATCCCAACGACAACAACCATTCAAAATGAACAAAGTTACATATGGAAAATGC 989
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GGAAGCATCCCAACGACAACAACCATTCAAAATGAACAAAGTTACATATGGAAAAATGC 960

Qy  990 CCCAAGTATATCAGCAAAACACTTAAAGCTGGCCACTGGGGATGAGGAATATACCAGA 1049
        |||||||||||||| |||||||||||||||||||||||||||||||||| ||||||||
Db  961 CCCAAGTATATCAGGCAAAACACTTAAAGCTGGCCACTGGGGATGAGGGATGTACCAGAA 1020

Qy 1050 AAGCAAATCAGA 1061
        ||||||||||||
Db 1021 AAGCAAATCAGA 1032
```

RESULT 9
AAQ29111
ID   AAQ29111 standard; DNA; 1762 BP.
XX
AC   AAQ29111;
XX
DT   25-MAR-2003 (revised)
DT   24-FEB-1993 (first entry)
XX

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Db      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    901 GGAAGCATCCCAACGACAACAACCATTCAAAATGAACAAAGTTACATATGGAAAATGC 960

Qy  990 CCCAAGTATATCAGCAAAACACTTAAAGCTGGCCACTGGGGATGAGGAATATACCAGA 1049
        |||||||||||||| |||||||||||||||||||||||||||||||||| ||||||||
Db  961 CCCAAGTATATCAGGCAAAACACTTAAAGCTGGCCACTGGGGATGAGGAATGTACCAGAA 1020

Qy 1050 AAGCAAATCAGA 1061
        ||||||||||||
Db 1021 AAGCAAATCAGA 1032
```

RESULT 8
AAZ47007
ID   AAZ47007 standard; DNA; 1698 BP.
XX
AC   AAZ47007;
XX
DT   29-FEB-2000 (first entry)
XX
DE   Equine influenza virus strain Newmarket 2/93 HA gene.
XX
KW   Antibacterial; antiviral; primer; RT-PCR; amplification; haemagglutinin;
KW   recombinant; vaccine; viral vector; pathogen; adjuvant; methacrylic acid;
KW   maleic anhydride; alkenyl derivative; animal; herpes virus; tetanus;
KW   influenza virus; feline leukemia; canine distemper; ss.
XX
OS   Equine influenza virus.
XX
PN   WO994633-A1.
XX
PD   10-SEP-1999.
XX
PF   01-MAR-1999;   99WO-FR000453.
XX
PR   03-MAR-1998;   98FR-00002800.
XX
PA   (MERI-) MERIAL.
XX
PI   Audonnet JF, Minke JM;
XX
DR   WPI; 2000-022918/02.
XX
PT   Live recombinant vaccine comprising viral vector and polymeric adjuvant,
PT   particularly directed against animal herpes and influenza viruses.
XX
PS   Example 5; Fig 1; 41pp; French.
XX
CC   This sequence represents the haemagglutinin (HA) gene from the equine
CC   influenza virus strain Newmarket 2/93. The gene was amplified and the
CC   product was used to generate a live recombinant vaccine which comprises:
CC   (1) a viral vector including, and expressing in vivo, a heterologous
CC   nucleotide sequence particularly a gene from a pathogen; and (2) at least
CC   one adjuvant, i.e. a (meth)acrylic acid polymer or a copolymer of maleic
CC   anhydride and alkenyl derivatives. The vaccines are used particularly to
CC   protect against animal herpes or influenza viruses, but also feline
CC   leukemia, tetanus and canine distemper
XX
SQ   Sequence 1698 BP; 619 A; 312 C; 372 G; 395 T; 0 U; 0 Other;

Query Match   92.7%; Score 984; DB 3; Length 1698;
Best Local Similarity   97.1%; Pred. No. 1.5e-267;
Matches 1002; Conservative   0; Mismatches   30; Indels   30; Gaps   0;

```
Qy   30 ATGAAGACAACAACAACAACAGCCACCATTATTTGATACTACTGACCCATTGGGTCTACA 89
        |||||||||||||           ||||||||||||||||||||||||||||||||||
Db    1 ATGAAGACAACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTACAAACCCACC 60

Qy   90 AGTGGAAACAACAACAGCCACCATTATGTCTGGGACACCACCATGCAGTAGCACAGAACATTG 149
        ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGTGGCAACAACACAGCCACCATTATGTCTGGGACACCACCATGCAGTAGCACAGAACATTG 120

Qy  150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
```

CC   prepare (simply by mixing components) and they do not involve any strong
CC   interactions between DNA and other components that are likely to cause
CC   complex formation. The vaccines are used to protect animals (pigs,
CC   horses, dogs, cattle, cats or birds) against a wide variety of viral or
CC   bacterial infections
XX
SQ   Sequence 1698 BP; 619 A; 312 C; 372 G; 395 T; 0 U; 0 Other;

Query Match   92.7%; Score 984; DB 2; Length 1698;
Best Local Similarity   97.1%; Pred. No. 1.5e-267;
Matches 1002; Conservative   0; Mismatches   30; Indels   0; Gaps   0;

Qy   30 ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC 89
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC 60

Qy   90 AGTGGAAACAACACAGCCACCATTATGTCTGGGACACCACGTAGCAAATGGAACATTG 149
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGTGGCAACAACACAGCCACCATTATGTCTGGGACACCACGTAGCAAATGGAACATTG 120

Qy   150 GTAAAAACAATAACGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 180

Qy   210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAAATGCACA 269
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   181 ATTTCAATAGGGAAAATATGCAACAACTCATATAGGGTTCTAGATGGAAGAAAATGCACA 240

Qy   270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTGATGAGAATTGGGAC 329
          |||||||||||||||||||||||||||||| ||||| ||| ||||||||||||||||||
Db   241 TTAATAGATGCAATGCTAGGAGACCCCCATTGTGATGATTTCAGTGATGAGAATTGGGAC 300

Qy   330 CTCTTCATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCTGACTAT 389
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTCTTCATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCTGACTAT 360

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   361 GCATCGCTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTCACAGCAGAGGGTTC 420

Qy   450 ACATGGACAGGTGTCACTCAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ACATGGACAGGTGTCACTCAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 480

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||| ||||||
Db   481 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAATTCTTACCCCATATTGAAT 540

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAAATATACATCTGGGGGATTCATCACCCG 629
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   541 GTGACAATGCCTAACAATAAAAATTTCGATAAATATACATCTGGGGGATTCATCACCCG 600

Qy   630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689
          ||||||||| || ||||||||||||| || |||| |||||||||||||||||||||||||
Db   601 AGCTCAAACAAAGAGCAGACAAATTATATATCCAAGAATCAGGACGAGTAACAGTCTCA 660

Qy   690 ACAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGTTAGGGGT 749
          |||| |||||||||||| || | ||||||| ||||||||||||||||||| ||||||
Db   661 ACAGAAGAGTCAACAAACAGTAATCCCTAACATCGGATCTAGACCGTGGGTCAGGGGT 720

Qy   750 CAATCAGGCAGGATAAGCATTACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
          ||||||||||||||||||||||||||||||||| ||||||||||||||||| ||||||||
Db   721 CAATCAGGCAGGATAAGCATTACTGGACCATTGTAAAACCTGGAGATATTCTAATGATA 780

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC 869
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   781 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC 840

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGTATTACCACCAAAT 929
          ||||||||||||||||||||||| |||||| |||||||||| |||||||||||||||||
Db   841 TCTGTAATGAGATCAGATGCACTCATAGACACTTGTGTCTGAATGTATTACCACCAAAT 900

Qy   930 GGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989

Qy   661 TCCAAGAATCAGGACGACGAGTAACAGTCTCAACACAAAAGAGAGTCAACAAACGATAGTCCCTA 720
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||| ||||| |||
Db   685 TCCAAGAATCAGGACGGCGAGTAACAGTCTCAACACAAAAGAGAGTCAACAAACAATAATCCCCA 744

Qy   721 ATATCGGATCTAGACCGTGGTTAGGGGTCAATCAGGCAGGATAAGCATTAATTACTGGACCA 780
          | |||||||||||||||||| || |||||||||||||||||||||||||||||||||||||
Db   745 ACATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCAGGATAAGCATTAATTACTGGACCA 804

Qy   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
          |||| ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   805 TTGTGAAAACCTGGAGATATTCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 864

Qy   841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACA 900
          |||||||||||||| || |||||||||||||||||||||||||||||||||||||||||
Db   865 GATATTTTAAATTGGAACAGGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACA 924

Qy   901 TTTGTGTCTGAATGTATTACCACCAAATGGAAGCATCCCCAACGACAAACCATTTCAA 960
          |||||||||| ||||||| ||||||||||||||||||||||||||||||||||||||
Db   925 CTTGTGTCTGAGTGTATTACACCACCAAATGGAAGCATCCCCAACGACAAACCATTTCAA 984

Qy   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAAACACTTTAAAGC 1020
          |||||||||||||||||||||||||||||||||||||||||||||| ||| |||| ||||
Db   985 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAGAATACTTTGAAGC 1044

Qy 1021 TGGCCACTGGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
          ||||||||||||||||||||| |||||| ||||||||||
Db 1045 TGGCCACTGGGATGAGGAATGTACCAGGAAAGCAAATCAGA 1085

RESULT 7
AA230211
ID   AA230211 standard; DNA; 1698 BP.
XX
AC   AA230211;
XX
DT   11-FEB-2000   (first entry)
XX
DE   Sequence of the haemagglutinin (HA) gene of EIV strain Newmarket 2/93.
XX
KW   Haemagglutinin gene; EIV; strain Newmarket 2/93; DNA vaccine; horse;
KW   acrylic acid polymer; methacrylic acid polymer; copolymer;
KW   maleic anhydride; alkenyl derivative; animal vaccine; viral infection;
KW   bacterial infection; ss.
XX
OS   Equine influenza virus.
XX
PN   FR2776928-A1.
XX
PD   08-OCT-1999.
XX
PF   03-APR-1998; 98FR-00004409.
XX
PR   03-APR-1998; 98FR-00004409.
XX
PA   (MERI-) MERIAL SAS.
XX
PI   Audonnet JCF, Minke JM;
XX
DR   WPI; 1999-593389/51.
XX
PT   Vaccine containing naked DNA and acrylic acid polymer or maleic anhydride
PT   copolymer, for protection against viral or bacterial diseases in animals.
XX
PS   Example 8; Fig 1; 34pp; French.
XX
CC   The present sequence represents the haemagglutinin gene of Equine
CC   influenza virus (EIV) strain Newmarket 2/93. The sequence was used to
CC   prepare a DNA vaccine for horses, representative of the DNA vaccines of
CC   the invention. The specification describes a DNA vaccine that comprises
CC   naked DNA encoding an antigenic polypeptide, and at least one adjuvant
CC   that is an acrylic or methacrylic acid polymer or a copolymer of maleic
CC   anhydride with an alkenyl derivative. The vaccines are simple and easy to

```
RESULT 6
AAQ04597
ID   AAQ04597 standard; DNA; 1797 BP.
XX
AC   AAQ04597;
XX
DT   25-MAR-2003;   (revised)
DT   02-OCT-1990;   (first entry)
XX
DE   Equine hemagglutinin H3 (EIV-A2).
XX
KW   Recombinant vaccines; equine influenza virus; haemagglutinin; H3;
KW   neuraminidase; N8; ss.
XX
OS   Equine influenza virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             54..1748
FT                   /*tag= a
FT                   /product= "EIV-A2 haemagglutinin H3"
FT   misc_RNA        102..1182
FT                   /*tag= b
FT                   /product= "N-terminal HA1 50kD portion"
FT   misc_RNA        1186..1748
FT                   /*tag= c
FT                   /product= "C-terminal HA2 27kD portion"
XX
PN   US4920213-A.
XX
PD   24-APR-1990.
XX
PF   21-JUL-1986;   86US-00888250.
XX
PR   20-JUN-1985;   85US-00747020.
XX
PA   (BIOT-) BIOTECH RES PARTNERS LTD.
XX
PI   Dale B, Cordell B;
XX
DR   WPI; 1990-163647/21.
DR   P-PSDB; AAR04943.
XX
PT   Recombinant vaccines against equine influenza virus - produced using DNA
PT   sequences encoding haemagglutinin and neuraminidase glyco-protein(s).
XX
PS   Disclosure; Page ?; 27pp; English.
XX
CC   There are nine neuraminidase (NA) subtypes and twelve haemagglutinin (HA)
CC   subtypes. The strain carrying H3N8 glycoproteins is designated equine
CC   influenza virus (EIV)-A2. The cDNA sequences encoding these will be
CC   useful in the construction of diagnostic probes for the disease and of
CC   probes for obtaining new cDNAs of the mutated form of the virus.
CC   Recombinant vaccines are produced.  See also AAQ04596-Q04599. (Updated on
CC   25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 1797 BP; 639 A; 341 C; 413 G; 404 T; 0 U; 0 Other;

Query Match             93.1%;  Score 987.4;  DB 2;  Length 1797;
Best Local Similarity   95.7%;  Pred. No. 1.6e-268;
Matches  1015;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        25 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA 84

Qy        61 CCCATTGGGTCTACAGTCAAAACCCACCAGTGAAACAACACAGCCACCACAATCATGTCTGG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        85 CCCATTGGGTCTACAGTCAAAACCCACCAGTGCAACAACCAGTGGCAACACAGTGGCTCGG 144

Qy       121 GACACCATGCAGTAGCAGAAAGTCTCTGTAATGATGAACATTTCAGAGCATTTCAGAGG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       145 GACACCATGCAGTAGCAGAAAGTCTCTGTAATGATGAACATTTGTGAAAAACAATTGAGG 204

Qy       181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAAATGCAACAACTCAT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       205 TGACAAATGCTACTGAATTAGTTCAGAGCACTTCAATAGGGAAAAATATGCAACAACCCAT 264

Qy       241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCGTAGGAGACCCCCACT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       265 ATAGGGTTCTAGATGGAAGAAACTGCACATTAATAGATGCAATGCGTAGGAGATCCCCACT 324

Qy       301 GTGATGTCTTCCAGTATGAGAATGGGACCTCCTCATAGAAGAGCAGCGCGCTTTCAGCA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       325 GTGATGTTTTTCAGTATGAGAATGGGACCCTCTTCATAGAAGAGCAGCGCGCTTTCAGCA 384

Qy       361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       385 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTTGTGGCATCTTCAG 444

Qy       421 GAACATTAGAATTCACAGCAGAGGGATTCACATGGACACAGTGTCACTCAAAACGGAAGAA 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       445 GAACATTAGAATTCACAGCAGAGGGATTCACATGGACACAGTGTCACTCAAAACGGAAGAA 504

Qy       481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTTTAGCCGACTGAATTGGCTAACAA 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       505 GTGGAGCCTGCAGAGAGGGGGTCAGCCGATAGTTCTTTTAGCCGACTGAATTGGCTAACAA 564

Qy       541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATTTCGACA 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       565 AATCTGGAAATTCTTACCCCACATTGAATGTAACAATGCCTAACAATAACAATTTCGATA 624

Qy       601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGAGAATTGTACA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       625 AACTATACATCTGGGGGATCCATCACCCCGAGCAACAAACAATGAGCAGAGAAATTGTATA 684

Qy       661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTA 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       685 TCCAAGAATCAGGGCGAGTAACAGTCTCAACAAAAGAAGTCAACAAACAATAATCCCCA 744

Qy       721 ATATCGGATCGACCGTGGGTTAGGGGTCAATCAGCAGGATAAGCATATACTGGGACCA 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       745 ACATCGGATCTAGACCGTGGGTCAATCAGCAGGATAAGCATATATTGGGACCA 804

Qy       781 TTGTAAAACCTGGAGATATCCTAATGATAAAGTAATGGCAACTTAGTTGCACCGGCCGGG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       805 TTGTGAAACCTGGAGATATCCTAATGATAAAGTAATGGCAACTTAGTTGCACCGGCCGGG 864

Qy       841 GATATTTTAAATTGAAAACAGGGAAAAGTCTGTAATGAGATCAGATGCACCCATAGACA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       865 GATATTTTAAAATCGAACAGGGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACA 924

Qy       901 TTTGTGTGTCTGAATGTATTACACCAAATGAAGCGCATCCCCAAGCGACAAACCATTTCAAA 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       925 CTTGTGTGTCCGAGTGTATTACACCAAATGAAGCGCATCCCCAAGCGACAAACCATTTAAAGC 984

Qy       961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       985 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAAGCAGAATACTTTGAAGC 1044

Qy      1021 TGGCCACTGGGATTGAGGAATATACCCAGAAAAGCAAATCAGA 1061
             |||||||||||||||||||||||||||||||||||||||||
Db      1045 TGGCCACTGGGATTGAGGAATGTACCAGAAAAGCAAATCAGA 1085
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FT   CDS              54..1748
FT                    /*tag= a
FT   mat_peptide      102..1082
FT                    /*tag= b
FT                    /label= HA 1
FT   mat_peptide      1086..1748
FT                    /*tag= c
FT                    /label= HA 2
XX
PN   WO8607593-A.
XX
PD   31-DEC-1986.
XX
PF   20-JUN-1986;    86WO-US001343.
XX
PR   20-JUN-1985;    85US-00747020.
XX
PA   (BIOT-) BIOTECHN RES PARTNE.
XX
PI   Dale B, Cordell B;
XX
DR   WPI; 1987-007191/01.
DR   P-PSDB; AAP70711.
XX
PT   Preventing equine influenza virus infection - using recombinant vaccines
PT   produced using DNA sequences encoding haemagglutinin and neuraminidase
PT   glyco:proteins.
XX
PS   Disclosure; Fig 2; 63pp; English.
XX
CC   Peptides derived from the haemagglutinin H7 and H3 and neuraminidase N7
CC   and N8 genes may be used to derive antigenic peptides useful in
CC   vaccination against equine influenza virus infection. Abs raised to the
CC   peptides may be used in diagnosis of the infection and construction of
CC   probes to mutated forms of the virus
XX
SQ   Sequence 1788 BP; 637 A; 340 C; 409 G; 402 T; 0 U; 0 Other;

Query Match             93.1%;  Score 987.4;  DB 1;  Length 1788;
Best Local Similarity   95.7%;  Pred. No. 1.6e-268;
Matches 1015;  Conservative   0;  Mismatches  46;  Indels   0;  Gaps   0;

Qy      1 AGCAAAAGCAGGGATATTTCTGTCAATCATGAGACAACCATTATTTGATACTACTGA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 AGCAAAAGCAGGGATATTTCTGTCAATCATGAGACAACCATTATTTGATACTACTGA 84

Qy     61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACACAGCCACCACCATTATGTCTGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGCAACACAGCCACCACCATTATGTCTGG 144

Qy    121 GACACCAGCTAGCAGCAGGGATTCAGACAACATTGGTAAAACAACAATAACTGATGACCAAAATTGAGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 GACACCAGCTAGCAGCAGGGATTCAGACAACATTGGTAAAACAACAATAACTGATGACCAAAATTGAGG 204

Qy    181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 TGACAAATGCTACTGAATTAGTTCAGAGCACTTCAATAGGGAAAATATGCAACAACCCAT 264

Qy    241 ATAAAGTTCTAGATGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300
          |||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 ATAGGGTTCTAGATGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGATCCCCACT 324

Qy    301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGAAGCAGCGCGCTTTCAGCA 360
          |||||||  ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GTGATGTTTTCNGTATGAGAATTGGGACCTCTTCATAGAAAGAAGAAGCAGCGCGCTTTCAGCA 384

Qy    361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTGGCATCTTCAG 444

Qy    421 GAACATTAGAATTCACAGCAGAGGATTCAGCAGGTCACTCAAAAACGGAAGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 GAACATTAGAATTCACAGCAGAGGATTCAGCAGGTCACTCAAAAACGGAAGAA 504
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(left-hand sequence continuation)

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Qy    241 ATAAAGTTCTAGATGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300
          |||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATAGGGTTCTAGATGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCACT 300

Qy    301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGAAGCAGCGCGCTTTCAGCA 360
          |||||||  ||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGATGTTTTCNGTATGAGAATTGGGACCTCTTCATAGAAAGAAGAAGCAGCGCGCTTTCAGCA 360

Qy    361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGCATCCTCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGCATCCTCAG 420

Qy    421 GAACATTAGAATTCACAGCAGAGAGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GAACATTAGAATTCACAGCAGAGAGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAA 480

Qy    481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540

Qy    541 AATCTTGGAAACTCTTACCCCACATTGAATGCTAACAATAACAATAAAAATTTCGACA 600
          ||||||||||| |||||||||| |||||||||||||||||||||||||||||||| |
Db    541 AATCTTGGAAATTCTTACCCCATATTGAATGCTAACAATAACAATAAAAATTTCGATA 600

Qy    601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACAACCAGCAGAGAATTGTACA 660
          ||||||||||||||||||||||||||||||||||||||||  ||||||  ||||||| |
Db    601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACAAACAGCAGACAAATTGTATA 660

Qy    661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAAGAGTCAACAACGATAGTCCCTA 720
          |||||||||||||||||||||||||||||||||  |||||||||||||  || ||||||
Db    661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAGAAAAGAGTCAACAACAGTAATCCCTA 720

Qy    721 ATATGGGATCTAGACCGTGGGTTAGGGGTTCAATCAGGCCAGGATAAGAAGCATATACTTACTGGACCA 780
          | ||  |||||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||||
Db    721 ACATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCCAGGATAAGAAGCATATACTTACTGGACCA 780

Qy    781 TTGTAAAACCTGGAGATATCCTAATGATAAAACAGTAATGCGAACTTAGTTGCACCGCGGG 840
          |||||||||||||||||||| ||||  |||||||||||||||||||||||||||||||||
Db    781 TTGTAAAACCTGGAGATATTCTAACCATAAACAGTAATGCGAACTTAGTTGCACCGCGCGGG 840

Qy    841 GATATTTTAAATTGAAAACAGGGGAAAGCTCTGTAATGAGAATCAGATGAGATCAGACCCATAGACA 900
          ||||||||||||||| |||||||||||||||||| ||||||||||| ||||||||||||| |||||
Db    841 GATATTTTAAATTGAGAACACAGGGGAAAGCTCTGTGTAATGAGATCAGTGCACCCATAGACA 900

Qy    901 TTTGTGTCTGAATGTATTACACCAAATGAAGCATCCCAACCACCAAACCATTTCAAA 960
          |||| ||||||| ||||||||||||||||||||||||||||||||||||||||| |||
Db    901 CTTGTGTCTGAATGTATTACACCAAATGAAGCATCCCAACCACCAAACCATTTCAA 960

Qy    961 ATGTGAACAAAGTTACATATGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGTGAACAAAGTTACATATGAAAATGCCCCAAGTATATCAGGCAAAACACTTTTAAAGC 1020

Qy   1021 TGGCCACTGGGATGAGGAATATACCAGAGAAAGCAAATCAGA 1061
          |||||| |||||||||||||||||||||||||||||||||||
Db   1021 TGGCCACCGGGATGAGGAATGTACCAGAGAAAGCAAATCAGA 1061
```

RESULT 5
AAN71067
ID   AAN71067 standard; DNA; 1788 BP.
XX
AC   AAN71067;
XX
DT   08-MAR-1991 (first entry)
XX
DE   Sequence encoding equine influenza virus strain H3N8 (EIV-A2)
DE   haemagglutinin protein H3.
XX
KW   HA; vaccine; Vaccina; ds.
XX
OS   Equine influenza virus.
XX
FH   Key   Location/Qualifiers

DT   25-MAR-2003 (revised)
DT   24-FEB-1993 (first entry)
XX
DE   EIV HA (A2/Suffolk/89).
XX
KW   Equine influenza virus; EIV; hemagglutinin; HA; A2/Suffolk/89;
KW   expression cassette; NYVAC; ALVAC; recombinant vector; M13;
KW   polymerase chain reaction; PCR; vaccinia virus; I3L promoter;
KW   canarypox virus; Copenhagen vaccine strain; virulence factor;
KW   deletion loci; recipient loci; ss.
XX
OS   Synthetic.
XX
PN   WO9215672-A1.
XX
PD   17-SEP-1992.
XX
PF   09-MAR-1992;   92WO-US001906.
XX
PR   07-MAR-1991;   91US-00666056.
PR   11-JUN-1991;   91US-00713967.
PR   06-MAR-1992;   92US-00847951.
XX
PA   (VIRO-) VIROGENETICS CORP.
XX
PI   Paoletti E, Perkus ME, Taylor J, Tartaglia J, Norton EK;
PI   Riviere M, De Taisne C, Limbach KJ, Johnson GP, Pincus SE, Cox WI;
PI   Francis J, Gettig RR;
XX
DR   WPI; 1992-331718/40.
XX
PT   Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating
PT   against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,
PT   mumps etc.
XX
PS   Disclosure; Fig 25; 456pp; English.
XX
CC   The sequence given encodes the equine influenza virus (EIV) hemagglutinin
CC   (HA) (A2/Suffolk/89). This sequence was used to generate an expression
CC   cassette for the insertion of the EIV HA gene into NYVAC and ALVAC
CC   recombinant vectors. The HA gene sequence was isolated by polymerase
CC   chain reaction from an M13 clone. Some non-conserved base-changes were
CC   observed due to the amplification process. The EIV HA gene was linked to
CC   the I3L promoter and inserted into a vaccinia insertion plasmid deleted
CC   for ORF's C6L-K1L. NYVAC is derived from a Copenhagen vaccine strain of
CC   vaccinia virus and ALVAC is derived from a canarypox virus which has been
CC   modified by deletion of non-essential regions of the genome encoding
CC   known or potential virulence factors. The deletion loci of both vectors
CC   were engineered as recipient loci for the insertion of foreign genes. See
CC   also AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 1762 BP; 637 A; 328 C; 384 G; 412 T; 0 U; 1 Other;

Query Match   96.0%; Score 1018.4; DB 2; Length 1762;
Best Local Similarity   97.5%; Pred. No. 2.8e-277;
Matches 1034; Mismatches 27; Conservative 0; Indels 0; Gaps 0;

Qy   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGA 60

Qy   61 CCCATTGGGTCTCACAGTCAAAACCCAACCAGTGAAACAACACAGCCACATTATGTCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCATTGGGTCTCACAGTCAAAACCCAACCAGTGAAACAACACAGCCACATTATGTCTGG 120

Qy   121 GACACCGCAGTAGCAGTAGCAAATGACAAATGGAACATTGGAGACATTGGAGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCGCAGTAGCAGTAGCAAATGACAAATGGAACATTGGAGACATTGGAGG 180

Qy   181 TGACAAATGCTACTACTGAATTAGTTCAGAGCATTCAGAGCATTTTGATACTACTGA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGACAAATGCTACTACTGAATTAGTTCAGAGCATTCAGAGCATTTTCAATAATGCAATCCAT 240

Db   61 AGTGGCAACAACAGCCACATTATGTCTCGGACACCATGCAGTAGCAAATGGAACATTG 120

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTACTGAATTAGTTCAGAGC 209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTACTGAATTAGTTCAGAGC 180

Qy   210 ATTTCAATAGGGAAAATATGCACAACTCATATAAGTTCTAGATGGAAGAAATTGCACA 269
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATTTCAATAGGGAAAATATGCAACAACTCATATAGAGTTCTAGATGGAAGAAATTGCACA 240

Qy   270 TTAATAGATGCAATGCTAGGAGGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTAATAGATGCAATGCTAGGAGGACCCCCACTGTGATGTCTTTCAGTATGAGAATTGGGAC 300

Qy   330 CTCCTCATAGAAAGAAGCAGCGCGTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTCCTCATAGAAAGAAGCAGCAGCGCGTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 360

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTGGAATTCACAGCAGAGGGATTC 420

Qy   450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 480

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTGAAT 569
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTGAAT 540

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAACTATACATCTGGGGGATTCATCACCCG 629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GTGACAATGCCTAACAATAAAAATTTCGACAACTATACATCTGGGGGATTCATCACCCG 600

Qy   630 AGCTCAAACCAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AGCTCAAACCAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 660

Qy   690 ACAAAAAGAAGTCAACAACGATAGTCCCTAATATCGGATCTCAGACCGTGGGGT 749
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ACAAAAAGAAGTCAACAACGATAATCCCTAATATCGGATCTCAGACCGTGGGGT 720

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATA 780

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAAAACAGGGAAAGC 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 AACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAAAACAGGGAAAGC 840

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACACATTTGTGTCTGAATGTATTACACCAAAT 929
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TCTGTAATGAGATCAGATGCACCCATAGACACATTTGTGTCTGAATGTATTACACCAAAT 900

Qy   930 GGAAGCATCCCCAACGACACAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GGAGCATCCCCAACGACACAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 960

Qy   990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGAATATACCAGAA 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGAATGTACCAGAA 1020

Qy   1050 AAGCAAATCAGA 1061
          ||||||||||||
Db   1021 AAGCAAATCAGA 1032

RESULT 4
AAQ29112
ID   AAQ29112 standard; DNA; 1762 BP.
XX
AC   AAQ29112;
XX

CC   or treating infections caused by influenza A viruses in animals,
CC   particularly horses. The present sequence is a DNA (neiwtHA1762) encoding
CC   wild type equine influenza virus H3N8 haemagglutinin (HA) protein denoted
CC   as PeiwtHA565. This sequence is modified to generate cold-adapted equine
CC   influenza virus
XX
SQ   Sequence 1762 BP; 639 A; 334 C; 383 G; 406 T; 0 U; 0 Other;

Query Match   97.3%; Score 1032.2; DB 3; Length 1762;
Best Local Similarity   98.3%; Pred. No. 3.5e-281;
Matches 1043; Conservative   0; Mismatches 18; Indels   0; Gaps   0;

Qy   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA 60
          ||||||||||||||||||| |||||||||||||||||||||||||| |||||||||||||
Db   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACCACTGA 60

Qy   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAAACAACACAGCCACATTATGTCTGG 120
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACAACACAGCCACATTATGTCTGG 120

Qy   121 GACACCATGCAGTAGCAACAGAAATGGAACATTGGTAAAACAATAACTGATGACCAAATTGAGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCAGTAGCAACAGAAATGGAACATTGGTAAAACAATAACTGATGACCAAATTGAGG 180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240

Qy   241 ATAAAGTTCAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCCACT 300
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATAGAGTTCAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCCACT 300

Qy   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTTCTTCATAGAAGAAGAGCAGCGCCTTCAGCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTGATGTCTTCAGTATGAGAATTGGGACCTTCTTCATAGAAGAAGAGCAGCGCCTTCAGCA 360

Qy   361 ATTGCTACCCATATGACATCCCGACTATGCATCGGTCCGGTCAGTAGCATCCTCAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTGCTACCCATATGACATCCCGACTATGCATCGGTCCGGTCAGTAGCATCCTCAG 420

Qy   421 GAACATTAGAATTCACAGCAGAGGATTCACATGACAGTGTCACTCAAAACCGAAGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAACATTGGAATTCACAGCAGAGGATTCACATGACAGTGTCACTCAAAACGAAGAA 480

Qy   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTAGCCGACGAATTGGCTAACAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGGATCCTGCAAAAGGGGATCAGCCGATAGTTTCTTAGCCGACGAATTGGCTAACAG 540

Qy   541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACATAAAATTTCGACA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACATAAAATTTCGACA 600

Qy   601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGAGAATTGTACA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAAAGAGCAGCAAAATTGTACA 660

Qy   661 TCCAAGAATCAGGAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCCAAGAATCGGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACAATAATCCCTA 720

Qy   721 ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGCCAGGATAAGCATATACTGGACCA 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACATCGGATCCAGACCGCGGGGTCAGGGTCAATCAGCCAGGATAAGCATATACTGGACCA 780

Qy   781 TTGTAAACCTGGAGATATCCTAATGATAAACAGTAATGCAACTTAGTTGCACCGGGGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   781 TTGTAAACCTGGAGATATCCTAATGATAAACAGTAATGCAACTTAGTTGCACCGGGGG 840

Qy   841 GATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAAAGCTCTGTAATGAGTGCACCCATAGACA 900
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Db   841 GATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAAAGCTCTGTAATGAGTGCACCCATAGACA 900

Qy   901 TTTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAAGCACAAAACCATTTCAAA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAAGCACAAAACCATTTCAAA 960

Qy   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy   1021 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
          |||||||||||||||||||||||||||||||||||||||||
Db   1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061

RESULT 3
AAZ30213
ID   AAZ30213 standard; DNA; 1698 BP.
XX
AC   AAZ30213;
XX
DT   11-FEB-2000 (first entry)
XX
DE   Sequence of the haemagglutinin (HA) gene of EIV strain Kentucky 1/94.
XX
KW   Haemagglutinin gene; EIV; strain Kentucky 1/94; DNA vaccine; horse;
KW   acrylic acid polymer; methacrylic acid polymer; copolymer;
KW   maleic anhydride; alkenyl derivative; animal vaccine; viral infection;
KW   bacterial infection; ss.
XX
OS   Equine influenza virus.
XX
PN   FR2776928-A1.
XX
PD   08-OCT-1999.
XX
PF   03-APR-1998;   98FR-00004409.
XX
PR   03-APR-1998;   98FR-00004409.
XX
PA   (MERI-) MERIAL SAS.
XX
PI   Audonnet JCF, Minke JM;
XX
DR   WPI; 1999-593389/51.
XX
PT   Vaccine containing naked DNA and acrylic acid polymer or maleic anhydride
PT   copolymer, for protection against viral or bacterial diseases in animals.
XX
PS   Example 9; Fig 2; 34pp; French.
XX
CC   The present sequence represents the haemagglutinin gene of Equine
CC   influenza virus (EIV) strain Kentucky 1/94. The sequence was used to
CC   prepare a DNA vaccine for horses, representative of the DNA vaccines of
CC   the invention. The specification describes a DNA vaccine that comprises
CC   naked DNA encoding an antigenic polypeptide, and at least one adjuvant
CC   that is an acrylic or methacrylic acid polymer or a copolymer of maleic
CC   anhydride with an alkenyl derivative. The vaccines are simple and easy to
CC   prepare (simply by mixing components) and they do not involve any strong
CC   interactions between DNA and other components that are likely to cause
CC   complex formation. The vaccines are used to protect animals (pigs,
CC   horses, dogs, cattle, cats or birds) against a wide variety of viral or
CC   bacterial infections
XX
SQ   Sequence 1698 BP; 618 A; 320 C; 369 G; 391 T; 0 U; 0 Other;

Query Match   96.1%; Score 1019.2; DB 2; Length 1698
Best Local Similarity   99.2%; Pred. No. 1.6e-277;
Matches 1024; Conservative   0; Mismatches 8; Indels   0; Gaps   0;

Qy   30 ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCAACC 89
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   1 ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCAACC 60

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCATGCAGTAGCACCATTG 149
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||

```
XX
PS   Claim 8; Page 89-92; 127pp; English.
XX
CC   The patent discloses experimentally generated cold-adapted equine
CC   influenza viruses, and reassortant influenza A viruses comprising at
CC   least one genome segment of the cold-adapted virus, which confers at
CC   least one identifying phenotype selected from cold-adaptation,
CC   temperature sensitivity, dominant interference and attenuation. These
CC   viruses are used in therapeutic compositions e.g. vaccines for preventing
CC   or treating infections caused by influenza A viruses in animals,
CC   particularly horses. The present sequence is a DNA (neicalHA1762)
CC   encoding cold-adapted equine influenza virus H3N8 haemagglutinin (HA)
CC   protein denoted as PeicalHA565. This sequence is a modified form of the
CC   wild type sequence
XX
SQ   Sequence 1762 BP; 641 A; 333 C; 381 G; 407 T; 0 U; 0 Other;

Query Match             97.4%;   Score 1033.8; DB 3; Length 1762;
Best Local Similarity   98.4%;   Pred. No. 1.2e-281;
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy     1 AGCAAAGCAGGGATATTTCTGTCAATCATGAGAGCAACCATTATTTTGATACTACTGA 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGCAAAGCAGGGATATTTCTGTCAATCATGAGAGCAACCATTATTTTGATACTACTGA 60

Qy    61 CCCATTGGGTCTCACAGTCAAAACCCACCAGTGAAACAACACAGCCACATTATGTCTGG 120
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Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATGGGAAAATATGCAACAACTCAT 240
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Qy   241 ATAAAGTTCTAGATGGAAGAAATGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
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Qy   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTTCTTCATAGAAGAAGCAGCCGCTTTCAGCA 360
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Qy   361 ATTGCTACCCATATGACATCCCTGACTAGTGCCATGCGTCCGGTCCATTGTAGCATCCTCAG 420
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Db   361 GTTGCTACCCATATGACATCCCTGACTAGTGCCATGCGTCCGGTCCATTGTAGCATCCTCAG 420

Qy   421 GAACATTAGAATTCACAGCAGAGGGATTCACATGGCAACAGGTGTCACTCAAAACGGGAAGAA 480
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Qy   481 GTGGAGCCTGCAAAAGGGGATCAGCCGGATAGTTCTTCTTTAGCCGACTGAATTGGCTAACAA 540
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Qy   541 AATCTGGAAACTCTTACCCCACATTGAAATGCAACAATGCCTAACAATAAAAATTTCGACA 600
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Db   541 AATCTGGAAACTCTTACCCCACATTGAAATGTGACAATGCCTAACAATAAAAATTTCGACA 600

Qy   601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGATTGTACA 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACAAGAGCAGACAAAATTGTACA 660

Qy   661 TCCAAGAATCAGGACGACGAGTAACAGTCTCAACAAAAAGAAGTCAACAAACGATAGTCCCTA 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCCAAGAATCAGGACGACGAGTAACAGTCTCAACAAAAAGAAGTCAACAAACAATAATCCCTA 720

Qy   721 ATATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780

Qy   781 TTGTAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTGTAAACCTGGAGATATCCTAACAGTAATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840

Qy   841 GATATTTAAATGAAAACAGGGAAAAGCTCTGTAATGAACATCAGATGCACCCATAGACA 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACA 900

Qy   901 TTTGTGTGTCTGAATGTATTACACCAAATGGAGCATCCCACGACACAACATTTCAA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTTGTGTGTCTGAATGTATTACACCAAATGGAGCATCCCACGACAACACATTTCAA 960

Qy   961 ATGTGAACAAAGTTACATATGCAGAAAATGCCCCAAGTATATCAGGCAAAAACACTTTAAAGC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATGTGAACAAAGTTACATATGCAGAAAATGCCCCAAGTATATCAGGCAAAAACACTTTAAAGC 1020

Qy  1021 TGGCCACTGGGATGAGGAATATACCAGAAAAAGCAAATCAGA 1061
         |||||||||||||||||||||||||||||||||||||||
Db  1021 TGGCCACTGGGATCGGGAATGTACCAGAAAAAGCAAATCAGA 1061

RESULT 2
AAZ50975
ID   AAZ50975 standard; DNA; 1762 BP;
XX
AC   AAZ50975;
XX
DT   05-JUN-2000   (first entry)
XX
DE   Wild type equine influenza virus H3N8 haemagglutinin protein DNA.
XX
KW   Haemagglutinin protein; wild type HA protein; horse; cold-adaptation;
KW   reassortant virus; temperature sensitivity; dominant interference;
KW   attenuation; antiviral; vaccine; prevention; treatment;
KW   influenza A virus infection; ds.
XX
OS   Equine influenza virus H3N8.
XX
FH   Key             Location/Qualifiers
FT   CDS             30..1727
FT                   /tag= a
FT                   /product= "HA protein"
FT                   /note= "The coding region without the stop codon is
FT                   specifically claimed"
XX
PN   WO20009702-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999;   99WO-US018583.
XX
PR   13-AUG-1998;   98US-00133921.
XX
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Dowling PW, Youngner JS;
XX
DR   WPI; 2000-224339/19.
DR   P-PSDB; AAY70056.
XX
PT   New cold-adapted equine influenza viruses and reassortant viruses used as
PT   vaccines for treating influenza infections in animals, particularly
PT   horses, have a phenotype such as temperature sensitivity or dominant
PT   interference.
XX
PS   Claim 8; Page 82-85; 127pp; English.
XX
CC   The patent discloses experimentally generated cold-adapted equine
CC   influenza viruses, and reassortant influenza A viruses comprising at
CC   least one genome segment of the cold-adapted virus, which confers at
CC   least one identifying phenotype selected from cold-adaptation,
CC   temperature sensitivity, dominant interference and attenuation. These
CC   viruses are used in therapeutic compositions e.g. vaccines for preventing
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
            Maximum Match 100%
            Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1033.8	97.4	1762	3	AAZ50976	Aaz50976 Cold-adap
2	1032.2	97.3	1762	3	AAZ50975	Aaz50975 Wild type
3	1019.2	96.1	1698	2	AAZ30213	Aaz30213 Sequence
4	1018.4	96.0	1762	2	AAQ29112	Aaq29112 EIV HA (A
5	987.4	93.1	1788	1	AAN71067	Aan71067 Sequence
6	987.4	93.1	1797	2	AAQ04597	Aaq04597 Equine he
7	984	92.7	1698	2	AAZ30211	Aaz30211 Sequence
8	984	92.7	1698	3	AAZ47007	Aaz47007 Equine in
9	976.2	92.0	1762	2	AAQ29111	Aaq29111 EIV HA (A
10	947.2	89.3	1698	2	AAV49391	Aav49391 EIV Fonta
11	607.2	57.2	1777	2	AAQ72855	Aaq72855 Full leng
12	601.6	56.7	1765	6	ABA93937	Aba93937 Influenza
13	598.4	56.4	1764	6	ABA93944	Aba93944 Influenza
14	585.6	55.2	1762	1	AAN70642	Aan70642 Sequence
15	566.2	53.4	1091	6	ABQ82724	Abq82724 Influenza
16	558.2	52.6	1653	6	ABQ82723	Abq82723 Influenza
17	556	52.4	987	6	ABQ82726	Abq82726 Influenza
18	554.4	52.3	987	6	ABQ82725	Abq82725 Influenza
19	549.2	51.8	1793	3	AAT59212	Aat59212 Influenza
20	549.2	51.8	1793	2	AAX00773	Aax00773 Influenza
21	549.2	51.8	1793	5	AAD09586	Aad09586 Influenza
22	546.4	51.5	988	12	ADO15237	Ado15237 Influenza
23	544.4	51.3	1757	2	AAT59216	Aat59216 Influenza
24	544.4	51.3	1757	2	AAX00777	Aax00777 Influenza
25	544.4	51.3	1757	5	AAD09590	Aad09590 Influenza
26	541.2	51.0	1701	5	AAV49298	Aav49298 SIV strai
27	541.2	51.0	1757	5	AAT59219	Aat59219 Influenza
28	541.2	51.0	1757	5	AAX00780	Aax00780 Influenza
29	541.2	51.0	1757	5	AAD09593	Aad09593 Influenza
30	150.4	14.2	1809	1	AAN71066	Aan71066 Sequence
31	148.2	14.2	1809	2	AAQ04596	Aaq04596 Equine he
32	148.2	14.0	1759	2	AAQ29110	Aaq29110 EIV HA (A
33 c	133.4	12.6	2005	3	AAA75002	Aaa75002 Nucleotid
34	133.4	12.6	4610	3	AAA75005	Aaa75005 Nucleotid
35	133.4	12.6	4930	3	AAA75000	Aaa75000 Nucleotid
36	127.2	12.0	1721	2	ADH29821	Adh29821 Swinepox
37	127.2	12.0	1721	2	AAV26247	Aav26247 Genomic D
38	125.2	11.8	1711	6	AAL50113	Aal50113 Recombina
39	123.8	11.7	1742	1	AAN00004	Aan00004 Sequence
40	123.6	11.6	1733	10	ADF28972	Adf28972 Influenza
41	122.6	11.6	1775	12	ADO15246	Ado15246 Influenza
42	122.4	11.5	1110	2	AAQ72807	Aaq72807 DNA encod
43	121.4	11.4	1724	2	AAA76188	Aaa76188 Swine inf
44	117.4	11.1	1701	2	AAV49294	Aav49294 SIV strai
45	116.2	11.0	1692	12	ADO15232	Ado15232 Influenza

ALIGNMENTS

RESULT 1
AAZ50976
ID   AAZ50976 standard; DNA; 1762 BP.
XX
AC   AAZ50976;
XX
DT   05-JUN-2000 (first entry)
XX
DE   Cold-adapted equine influenza virus H3N8 haemagglutinin protein DNA.
XX
KW   Haemagglutinin protein; modified HA protein; horse; cold-adaptation;
KW   reassortant virus; temperature sensitivity; dominant interference;
KW   attenuation; antiviral; vaccine; prevention; treatment;
KW   influenza A virus infection; ds.
XX
OS   Equine influenza virus H3N8.
XX
FH   Location/Qualifiers
FT   Key
FT   CDS   30. .1727
FT   /*tag= a
FT   /product= "HA protein"
FT   /note= "The coding region without the stop codon is
FT   specifically claimed"
XX
PN   WO200009702-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999; 99WO-US018583.
XX
PR   13-AUG-1998; 98US-00133921.
XX
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Dowling PW, Youngner JS;
XX
DR   WPI; 2000-224339/19.
DR   P-PSDB; AAY70057.
XX
PT   New cold-adapted equine influenza viruses and reassortant viruses used as
PT   vaccines for treating influenza infections in animals, particularly
PT   horses, have a phenotype such as temperature sensitivity or dominant
PT   interference.

DB:

US-10-826-929A-1 (1-1061) x US-10-105-232-284 (1-39)

```
Qy    858 ACAGGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGT 917
           |||||||||||||||||||||||||||||||||||||||||   |||  |||||||||
Db      2 ThrGlyLysSerSerValMetArgSerAspAlaProIleAspPheCysAsnSerGluCys 21

Qy    918 ATTACACCAAATGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAA 971
           ||||||||||||  |||||||||||||||||||||||||||||||||||||
Db     22 IleThrProAsnGlnSerIleProAsnAspLysProPheGlnAsnValAsnLys 39
```

           14   Gaps: 0

Search completed: February 27, 2005, 18:56:49
Job time : 166.5 secs

```
Db        357 Leu 357

RESULT 14
US-10-676-909-90
; Sequence 90, Application US/10676909
; Publication No. US20040008521A1
; GENERAL INFORMATION:
;  APPLICANT: KROPSHOFER, H.
;  APPLICANT: VOGT, A.
;  TITLE OF INVENTION: Method for the identification of antigenic peptides associated to
;  TITLE OF INVENTION: diseases
;  FILE REFERENCE: 21388
;  CURRENT APPLICATION NUMBER: US/10/676,909
;  CURRENT FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: EP 02022223.8
;  PRIOR FILING DATE: 2002-02-10
;  NUMBER OF SEQ ID NOS: 90
;  SEQ ID NO 90
;  SOFTWARE: PatentIn version 3.2
;  LENGTH: 346
;  TYPE: PRT
;  ORGANISM: Influenza B virus
US-10-676-909-90

Alignment Scores:
Pred. No.:              2.17e-11          Length:          346
Score:                  205.00            Matches:         88
Percent Similarity:     39.29%            Conservative:    55
Best Local Similarity:  24.18%            Mismatches:      149
Query Match:            10.72%            Indels:          72
DB:                                       Gaps:            19

US-10-826-929A-1 (1-1061) x US-10-676-909-90  (1-346)

Qy  111 TTATGTCTGGGACCACCATGCAGTAGCAAATGGAACATTGTAAAAACAATAACTGATGAC 170
            :::||||       ::     ::: :||||||||||
Db    3 IleCysThrGlyIleThrSerSerAsnSerProHisValValLysThrAlaThrGlnGly 22

Qy  171 CAAATTGAGGTGACAAATGCTACTGAATTAGTTCAG------------------------ 206
            ::::::  ||||||       |||
Db   23 GluValAsnValThrGlyValIleProLeuThrThrProThrLysSerHisPheAla 42

Qy  207 --------------AGCATTTCAATAGGGAAAATGCAAACAACTCATATAAAGTTCTAGAT 254
                       ::: ::  |||||||:::|||
Db   43 AsnLeuLysGlyThrLysThrArgGlyLysLeuCysProThrCysLeu----------- 58

Qy  255 GGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACTGT---GATGTCTTC 311
             ||||||       ||||||        ||||||||       :||
Db   59 -----AsnCysThrAspLeuAspValAlaLeuGlyArgProMetCysValGlyValThr 76

Qy  312 CAGTATGAGAATTGGGACCTCTTCATAGAAAAGAAGCAGCCGCTTCAGCAATTGCTACCCA 371
                  ::: |||||||       |||       :::|||:::||
Db   77 ProSerAlaLysAlaSerIleLeuHisGluValArgProValThrSerGlyCysPhePro 96

Qy  372 ------TATGACATCCCTGACTATGCATGCATGTCCGGTCCGGTCCATTGTAGCATCCTCAGGAACA 425
           ::::||         |||       :::::::
Db   97 IleMetHisAspArgThrLysIleArgGlnLeuProAsnLeuLeuArgGlyTyrGluLys 116

Qy  426 TTAGAATTCACACGACAGAGGGATTCACATGACCAGGTGTCACTCAAAC----------- 473
           |||       ::: |||  |||
Db  117 IleArgLeuSer-----------------ThrGlnAsnValIleAsnAla 127

Qy  474 ------------------------GGAAGAAGTGGAGCCTGCAAAAGGGGATCA 503
                                    ||| |||||||:::|||      :::
Db  128 GluLysAlaProGlyGlyProTyrArgLeuGlyThrSerGlySerCysProAsnAlaThr 147

Qy  504 GCCGATAGT---TTCTTTAGCCGACTGAATTGG---CTAACAAAATCTGGAAACTCTTAC 557
           ::: |||||||:::   ::: ||| |||
Db  148 SerArgSerGlyPhePheAlaThrMetAlaTrpAlaValProLysAspAsnAsnLysThr 167

Qy  558 CCCACA------TTGAATGTGACAATGCCTAAC----AATAAAAATTTCGACAAACTA 605
           ||| ||| |||       :::||:::
Db  168 AlaThrAsnProLeuThrValGluValProHisIleCysThrLysGluGluAspGlnIle 187
```

```
Qy  606 TACATCTGGGGGATTCATCACCCGAGCTCAACCAACAGAGACAGAGAATTGTACATCCAA 665
            |||||        ::: :||||||
Db  188 ThrValTrpGlyPheHisSerAspAsnLysThrGlnMetLys---AsnLeuTyrGlyAsp 206

Qy  666 GAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACG--ATAGTCCTAAT 722
            ::: :  ||||||||  |||
Db  207 SerAsnProGlnLysPheThrSerSerAlaAsnGlyValThrHisTyrValSerGln 226

Qy  723 ATCGGATCTAGACCG-----------------TGGGTTAGGGTCAATCAGGCAGGATAAGC 767
           |||||        |||||||
Db  227 IleGlyGlyPheProAspGlnThrGluAspGlyGlyLeuProGlnSerGlyArgIleVal 246

Qy  768 ATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATAAACAGTAATGGCAACTTA 827
            ::: :     ||||||||       :::
Db  247 ValAspTyrMetValGlnLysProGly-------------LysThrGlyThrIle 260

Qy  828 GTTGCACCGCGGGGATATTTAAA------------------TTGAAAACAGGAAAAGCTCT 872
           |||       |||||       :::|||:::|||
Db  261 ValTyrGlnArgGlyIleLeuLeuProGlnLysValTrpCysAlaSerGlyArgSerLys 280

Qy  873 GTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGTATTACCACCAAAT--- 929
           |||:::||        ||||||:::||
Db  281 ValIleLysGlySerLeuProLeu---IleGlyGluHisAspCysSerLeuHisGluLysTyr 299

Qy  930 GGAAGCATCCCCAACGACAACCA---TTTCAAAATGTGACAAAGTTACATATGGAAAA 986
           ||| :::                  |||
Db  300 GlyGlyLeuAsnLysSerLysSerProTyrTyrThrGlyGluHisAlaAlaIleGlyAsn 319

Qy  987 TGCCCCAAGTATATCAGGCAAAACACTTTAAAGCTGACATCGGCCACTGGCGGATGAGAATATACCA 1046
           |||||||||||||||||||||
Db  320 CysProIleTrpValLys---ThrProLeuLysLeuAlaAsnGlyThrLysThrLysArgPro 338

Qy 1047 GAAAAGCAAATC 1058
           ::::::
Db  339 ProAlaLysLeu 342
```

```
RESULT 15
US-10-105-232-284
; Sequence 284, Application US/10105232
; Publication No. US2003018O328A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT: BOGOCH, ELENORE S.
;  TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
;  TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
;  FILE REFERENCE: 09425-46904
;  CURRENT APPLICATION NUMBER: US/10/105,232
;  CURRENT FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/146,755
;  PRIOR FILING DATE: 1998-09-04
;  PRIOR APPLICATION NUMBER: 09/817,144
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 08/198,139
;  PRIOR FILING DATE: 1994-02-17
;  NUMBER OF SEQ ID NOS: 535
;  SOFTWARE: PatentIn 2.1
;  SEQ ID NO 284
;  LENGTH: 39
;  TYPE: PRT
;  ORGANISM: Influenza virus
US-10-105-232-284

Alignment Scores:
Pred. No.:              1.55e-09          Length:          39
Score:                  184.00            Matches:         35
Percent Similarity:     92.11%            Conservative:    0
Best Local Similarity:  92.11%            Mismatches:      3
Query Match:            9.62%             Indels:          0
```

```
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 729
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 270
;  LENGTH: 47
;  TYPE: PRT
;  ORGANISM: Influenza virus
US-10-189-437-270

Alignment Scores:
Pred. No.:               1.3e-13
Score:                   225.00
Percent Similarity:      91.30%
Best Local Similarity:   89.13%
Query Match:             11.77%
DB:                      14

US-10-826-929A-1 (1-1061) x US-10-189-437-270  (1-47)

Qy    858  ACAGGGAAAAGCTCTGTAATGAGATCAGATGACCACCATAGACATTTGTGTCTCGAATGT  917
               ||||||||||||||||||||||||||||||||||||||||||   ||| |||||||||
Db      2  ThrGlyLysSerSerValMetArgSerAspAlaProIleAspPheCysAsnSerGluCys  21

Qy    918  ATTACCACCAAATGGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACA  977
               ||||||||||||  |||||||||||||||||||||||||||| |||||||||||::|||
Db     22  IleThrProAsnGlnSerIleProAsnAspLysProPheGlnAsnValAsnLysIleThr  41

Qy    978  TATGGAAAATGCCCCAAG  995
               ||||||||||||||||||
Db     42  TyrGlyAlaCysProLys  47


RESULT 13
US-10-381-530-30|
;  Sequence 30, Application US10381530
;  Publication No. US2004013701A1
; GENERAL INFORMATION:
;  APPLICANT: KATINGER, Hermann
;  APPLICANT: EGOROV, Andre
;  APPLICANT: FERKO, Boris
;  APPLICANT: ROMANOVA, Julia
;  APPLICANT: KATINGER, Dietmar
;  TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE
;  FILE REFERENCE: P/167-134
;  CURRENT APPLICATION NUMBER: US/10/381,530
;  CURRENT FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: PCT/EP01/11087
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: 00120896.6
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;  LENGTH: 584
;  TYPE: PRT
;  ORGANISM: Influenza B/Vienna/1/99/ca
US-10-381-530-30

Alignment Scores:
Pred. No.:               4.97e-13
Score:                   222.00
Percent Similarity:      39.11%
Best Local Similarity:   23.10%
Query Match:             11.61%
DB:                      16

US-10-826-929A-1 (1-1061) x US-10-381-530-30  (1-584)

Qy     30  ATGGAGAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCTACAGTCAAAACCCCACC  89
               |||||| ||::||||::||::||
Db      1  MetLysAlaIleIleValLeuLeuMetValVal----------------------------  11

Qy     90  AGTGGAAACAACACAGCCACCATTATGTCTGGGACACCATGCAGTAGCAGTAGAACATTG  149
               :::
```

```
;::|||                                              :::   :::
12  ---ThrSerAsnAlaAspArgIleCysThrGlyIleThrSerSerAsnSerProHisVal  30

150 GTAAAAACAATAACTGATGACCAAATTGAGTGAGTGCAAATGCTACTGAATTAGTTCAG---  206
    |||||||||   :::::  :::::|||  :::::| |||  |||
31  ValLysThrAlaThrArgIleGlnGlyValAlaAsnValThrGlyAlaIleProLeuThrThrThr  50

207 ------------------------------------AGCATTCAATAGGGAAAAATATGCAAC  233
                                        ::: ::: |||||||||| |||
51  ProThrLysSerHisPheAlaAsnLeuLysGlyThrLysThrArgGlyLysLeuCysPro  70

234 AACTCATATAAAGTTCTAGATGAGGAAGAAATTGACATTATAGATGCAATGCTAGGAGAC  293
    |||||||||||        :::|||||||| |||||  ||||
71  ThrCysLeu--------------::---AsnCysThrAspLeuArgValAlaLeuGlyArg  84

294 CCCCACTGT---GATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGC  350
    ||| |||            :::                        |||
85  ProMetCysValGlyLysIleThrProSerAlaLysAlaSerIleLeuHisGluValArgPro  104

351 GCTTTCAGCAATTGCTACCCA------TATGACATCCCTGACTATGCATCGCTCCGGTCC  404
    |||||||||  ||||||||||||                      :::
105 ValThrSerGlyCysPheProIleMetHisAspArgThrLysIleArgGlnLeuProAsn  124

405 ATTGTAGCATCCTCAGGACATCAGGAATTCACAGCAGAGGGGATTCACATGGACA------  458
    :::::::                  :::  :::  |||
125 LeuLeuArgGlyTyrGluLysSerThrGlnAsnValIleAsnThrGluLys  144

459 -------------GGTGTCACTCAAAACCGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT  509
                  |||  ::: |||||||||:::|||  :::::
145 AlaProGlyGlyProTyrArgLeuGlyThrSerGlyGlySerCysProAsnAlaThrSerLys  164

510 AGT---TTCTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTACCCACCATTG  566
    |||||| :::|||         |||||       :::
165 SerGlyPhePheAlaThrMetAlaThrpAlaValProArgAspAsnLysThrAlaThr  184

567 AAT-----GTGACAATGCCTAAC------AATAAAAATTTCGACAAACTATACATC  611
    |||        |||:::||||||                :::    :::
185 AsnProLeuThrValGluValProHisIleCysThrLysGlyGlnIleGlnThrVal  204

612 TGGGGGATTCATCACCCGAGCTCAAACCACCAGACAGAGAATTGTACATCCAAGAATCA  671
    |||||| |||  :::          ::::::    :::
205 TrpGlyPheHisSerAspAsnLysThrGlnMetLysAsnLeuTyrGlyAspSerAsnPro  224

672 GGAGAGTAACAGTCTCAACAAAAAGAAGTCAACAAACGATAGTCCTAATATCGGATCT  731
    |||||||||||||||||||||
225 GlnLysPheThrSerSerAlaAsnGlyIleThrHisHisTyrValSerGlnIleGlyGly  244

732 AGACCG-------------TGGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGG  776
    |||||               ::: :::
245 PheProAspGlnThrGluAspGlyLeuProGlnSerGlyArgIleValValAspTyr  264

777 ACCATTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGACAACTTAGTTGCACCG  836
    |||||||||  |||||||||||:::|||::::||
265 MetValGlnLysProGly--------------------LysThrGlyThrIleValTyrGln  278

837 CGGGGGATATTTTAAA-------------------TTGAAAACAGGGAAAAGCTCTGTAATGAGA  881
    |||||||||::::::                      :::|||::::::
279 ArgGlyIleLeuLeuProGlnLysValTrpCysAlaSerGlyArgSerLysValIleLys  298

882 TCAGATGCACCCATAGACAGCATTGTGTGTGTCGAAATGTATTACACCAAAT---GGAAGCATC  938
    |||||||::::  :::::|||::::::||||::                   |||  |||
299 GlySerLeuProLeu---IleGlyValAlaAspCysSerLeuHisGlyLysTyrGlyLeu  317

939 CCCAACGACAAACCA---TTTCAAAATGTGAACAAAGTTACATATGGAAAATGCCCCAAG  995
    |||||||||||              ::: ::: ||||||
318 AsnLysSerLysSerProTyrTyrThrGlyLeuHisAlaLysAlaIleGlyAsnCysProIle  337

996 TATATCAGGCAAAACACTTTAAAGCTGCCACTGGCATGGCGATGAGGAATATACCAGAAAAGCAA  1055
    :::::::::                             ::: :::
338 TrpValLys---ThrProLeuLysSerLeuAsnGlyThrLysTyrArgProProAlaLys  356

1056 ATC  1058
     :::
```

```
Query Match:            20.55%        Indels:    220
DB:                     9             Gaps:      2

US-10-826-929A-1 (1-1061) x US-09-918-568-58  (1-347)

Qy      30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAAC---CCA 86
           ||||||||||  ||      ||||||        |||:::  || |
Db       1 MetLysThrIleIleAlaLeuSerTyrIlePheCysLeuLeuAlaLeuGlyGlnLeuPro 20

Qy      87 ACCAGTGGAAACAACACAGCCACATTATGTCTGGGACACCACATTGCAGTAGCAAATGGAACA 146
           :::  ||||||||||||||||||
Db      21 GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyLeuHisAlaValProAsnGlyThr 40

Qy     147 TTGGTAAAAACAATAACTGATGACCAAATGAGGTGACAAATGCTACTGAATTAGTTCAG 206
           ||||||||||||||||
Db      41 LeuValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60

Qy     207 AGCATTTCAATAGGGGAAAATATGCAACACTCATATAAAGTTCTAGATGGAAGAAATTGC 266
           |||  |||  ||||||||
Db      61 SerSerSerThrGlyLysIleCysAsnAsn-------------------- 70

Qy     267 ACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGCTTCCAGTATGAGAATTGG 326
           -------
Db      70 ------------------------------------------------- 70

Qy     327 GACCTCTTCATAGAAGAAGAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGAC 386
           -------
Db      70 ------------------------------------------------- 70

Qy     387 TATGCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGCAGAGGGGA 446
           -------
Db      70 ------------------------------------------------- 70

Qy     447 TTCACAATGGACAGGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGGATCAGCC 506
           -------
Db      70 ------------------------------------------------- 70

Qy     507 GATAGTTTCTTTAGGCCGACTGAATTGGCTAACAAAAATCTGGAAACTCTTACCCCACCATTG 566
           -------
Db      70 ------------------------------------------------- 70

Qy     567 AATGTGACAATGCCTAACAATAAAAATTTCGACAACAATATACATCTGGGGATTCATCAC 626
           -------
Db      70 ------------------------------------------------- 70

Qy     627 CCGAGCTCAAACCAACCACAGACAGAATTGTACATCCAAGAATCAGGACCAGTAACAGTC 686
           -------
Db      70 ------------------------------------------------- 70

Qy     687 TCAACAAAAGAAGTCAACAAAACGATAAGTCCCTAATATCGGATCTAGACCGTGGGTTAGG 746
           -------
Db      70 ------------------------------------------------- 70

Qy     747 GGTCAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATG 806
           -------
Db      70 ------------------------------------------------- 70

Qy     807 ATAAACAGTAATGGCAACTTAGTTGCACCGGGGGATATTTTAAATTGAAAACAGGGAAA 866
           -------
Db      70 ------------------------------------------------- 70

Qy     867 AGCTCTGTGTAATGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTACACCA 926
           ||||||||||||||||
Db      71 -----------IleAspThrCysIleSerSerGluCysIleThrPro 81

Qy     927 AATGGAAGCATCCCCACCAGACAAACCCATTCAAAATGTGAACAAAGTTACATATGAAAA 986
           ||||||||  ||||::||||||||
Db      82 AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla 101

Qy     987 TGCCCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCA 1046
           |||:::||||::||
Db     102 CysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValPro 121
```

```
Qy    1047 GAAAAGCAAATCAGA 1061
           ||||||||   |||
Db     122 GluLysGlnThrArg 126
```

RESULT 11
US-10-105-232-283
; Sequence 283, Application US/10105232
; Publication No. US2003018032BA1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
;
; SEQ ID NO 283
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Influenza virus
US-10-105-232-283

Alignment Scores:
Pred. No.:   Length: 47
Score: 1.3e-13   Matches: 41
Percent Similarity: 225.00   Conservative: 1
Best Local Similarity: 91.30%   Mismatches: 4
Query Match: 89.13%   Indels: 0
DB: 11.77%   Gaps: 0
                        14

US-10-826-929A-1 (1-1061) x US-10-105-232-283 (1-47)

Qy   858 ACAGGGAAAAGCTCTGTAATGACAGCTCTGTAATGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGT 917
           ||||||||||||||||||||||||||||||||||||||||||||
Db   2 ThrGlyLysSerSerValMetArgSerAspAlaProIleAspPheCysAsnSerGluCys 21

Qy   918 ATTACACCAAATGGAAGCATCCCCACGACCAAACCATTCAAAATGTGAACAAAGTTACA 977
           |||||||||||||||||||||||||||:::|||||
Db   22 IleThrProAsnGlnSerIleProAsnAspLysProPheGlnAsnValAsnLysIleThr 41

Qy   978 TATGAAAATGCCCCAAG 995
           |||||||||||||||||
Db   42 TyrGlyAlaCysProLys 47
```

RESULT 12
US-10-189-437-270
; Sequence 270, Application US/10189437
; Publication No. US2003019441A1 *
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09

```
Qy    345 AGCAGCGCTTCAGCAAT---TGCTACCCATATGACATCCTGACTATGCATCGCTCCGG 401
              :::          ||||||||       |||  |||  |||
Db     98 GluAsnProArgAspGlyLeuCysTyrProGlySerPheAsnAspTyrGluGluLeuLys 117

Qy    402 TCCATTGTTAGCATCCTCAGGAACATTAGAATTCACA------GCAGAGGGATTCACATGG 455
              :::||::::|||       |||
Db    118 HisLeuLeuSerValLysHisPheGluLysValLysIleLeuProLysAspArgTrp 137

Qy    456 ACAGGTGTCACTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGATCAGCCGATAGTTTC 515
              |||  ||||:::|||||       |||||
Db    138 ThrGlnHisThrThrGlySerArgAlaCysSerArgAlaValSerGlyAsnProSerPhe 157

Qy    516 TTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCACATTGAATGTGACA 575
              |||   :::  ||||:||||||          :::  ||||||
Db    158 PheArgAsnMetValTrpLeuThrLysSerGluSerAsnTyrProValAlaLysGlySer 177

Qy    576 ATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGATTCATCACCCGAGCTCA 635
              ||       |||           :::||:
Db    178 TyrAsnAsnThrSerGlyGluGlnMetLeuIleIleTrpGlyValHisHisProAsnAsp 197

Qy    636 AACCACAGCAGCAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCAACAAAA 695
              ::|||                |||  |||
Db    198 GluThrGluGlnArgThrLeuTyrGlnAsnValGlyThrTyrValSerValGlyThrSer 217

Qy    696 AGAAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGTCAATCA 755
              :::           ||:|||  ||:||||| |||  |||||
Db    218 ThrLeuAsnLysArgSerThrProAspIleAlaThrArgProLysValAsnGlyLeuGly 237

Qy    756 GGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATAAAACAGT 815
              :::                 ||||:||||       |||:::||||||
Db    238 SerArgMetGluPheSerTrpThrLeuLeuAspMetTrpAspThrIleAsnPheGluSer 257

Qy    816 AATGCGAACCTAGTTGCACCGCGGGGGATATTTTAAATTG---AAAACAGGGAAAAGCTCT 872
              ||||||||:::||||       |||  ||
Db    258 ThrGlyAsnLeuIleAlaProLeuTyrGlyPheLysIleSerLysArgGlyAsnSerGly 277

Qy    873 GTAATGAGATCAGATGCACCCAGACATTTGTGTCTCGAANGTATTACCACCAAATGGA 932
              :::||:::::::        |||      :::||||||         ||||||
Db    278 IleMetLysThrGluGlyThrLeuGluAsnCysGlnThrLysGluThrProLeuGly 297

Qy    933 AGCATCCCCAACGACAACCATTTCAAAATGTGAACAAAGTTACATGGAAAATGCCCC 992
              :::||          ||||||   |||:||       ||:::|||||||
Db    298 AlaIleAsnThrThrLeuProPheHisAsnValHisProLeuThrIleGlyGluCysPro 317

Qy    993 AAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAAAAG 1052
              ||||:::::::                |||||:::
Db    318 LysTyrValLysSerGluLysGluLeuValLeuAlaThrGlyLeuArgAsnValProGlnIle 337

Qy   1053 CAAATCAGA 1061
              :::  ||
Db    338 GluSerArg 340
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RESULT 10
US-09-918-568-58

; Sequence 58, Application US/09918568
; Patent No. US20020054882A1
; GENERAL INFORMATION:
;   APPLICANT: Yoshinobu OKUNO et al.
;   TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
;   ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
;   NUMBER OF SEQUENCES: 58
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
;   STREET: 2033 K Street, N.W., #800
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20006
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: WordPerfect 5.1

;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/918,568
;   FILING DATE: 02-Aug-2001
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/004,422
;   FILING DATE: January 8, 1998
;   APPLICATION NUMBER: 08/443,862
;   FILING DATE: May 22, 1995
;   APPLICATION NUMBER: 08/229,781
;   FILING DATE: April 19, 1994
;   APPLICATION NUMBER: 08/054,016
;   FILING DATE: April 29, 1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Warren M. Cheek, Jr.
;   REGISTRATION NUMBER: 33,367
;   REFERENCE/DOCKET NUMBER: <Unknown>
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-721-8200
;   TELEFAX: 202-721-8250
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 58:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 347 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: <Unknown>
;   ANTI-SENSE: <Unknown>
;   FRAGMENT TYPE: <Unknown>
;   ORIGINAL SOURCE:
;   ORGANISM: <Unknown>
;   STRAIN: <Unknown>
;   INDIVIDUAL ISOLATE: <Unknown>
;   DEVELOPMENTAL STAGE: <Unknown>
;   HAPLOTYPE: <Unknown>
;   TISSUE TYPE: <Unknown>
;   CELL TYPE: <Unknown>
;   CELL LINE: <Unknown>
;   ORGANELLE: <Unknown>
;   IMMEDIATE SOURCE:
;   LIBRARY: <Unknown>
;   CLONE: <Unknown>
;   POSITION IN GENOME:
;   CHROMOSOME/SEGMENT: <Unknown>
;   MAP POSITION: <Unknown>
;   UNITS: <Unknown>
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:
;   PUBLICATION INFORMATION:
;   AUTHORS:
;   TITLE:
;   JOURNAL:
;   VOLUME:
;   ISSUE:
;   PAGES:
;   DATE:
;   DOCUMENT NUMBER:
;   FILING DATE:
;   PUBLICATION DATE:
;   RELEVANT RESIDUES IN SEQ ID NO:
;   SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-918-568-58

Alignment Scores:
Pred. No.:   Length: 347
Score: 3.55e-30   Matches: 98
Percent Similarity: 393.00   Conservative: 9
Best Local Similarity: 31.01%   Mismatches: 18
                           28.41%

```
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3466
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Influenza A virus
US-10-224-999A-3466

Alignment Scores:
Pred. No.:            1.69e-44        Length:              412
Score:               536.50          Matches:             123
Percent Similarity:  54.02%          Conservative:         72
Best Local Similarity: 34.07%        Mismatches:          145
Query Match:         28.06%          Indels:               21
DB:                                  Gaps:                 10

US-10-826-929A-1 (1-1061) x US-10-224-999A-3466 (1-412)

Qy     6 AAGCAGGGGATATTTCTGTCAATCATGAGAGCAACCATTATTTGATACTACTGACCCAT 65
           |||  |||||  :::::  ||       |||     ::||||||||
Db     2 LysAlaGlyVal------ThrMetGluLysLeuLeuValIleAlaMetLeuLeu------ 17

Qy    66 TGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACACAGCCACCATTATGTCTGGGACAC 125
           |||   |||       ::||   ||   :::||||:::: ::
Db    18 --------------------AlaSerThrAsnAlaTyrAspArgIleCysIleGlyTyr 30

Qy   126 CATGCAGTAGCAAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGGTGACA 185
           :::              |||||  ||  |||  ::  |||     :::
Db    31 GlnSerAsnAsnSerThrAspThrValAsnThrLeuIleGluGlnAsnValProValThr 50

Qy   186 AATGCTACTGAATTAGTTCAGAGCATTCAATGGGAAAAATATGCAACAACTCATATAAA 245
           |||||||||||:::::::        |||||
Db    51 GlnThrMetGluLeuValGluThrGluLysHisProAlaTyrCysAsnThrAspLeuGly 70

Qy   246 GTT---CTAGATGGAAGAAATTGCACATTAATAGATGATGCAATGCTAGGAGACCCCCACTGT 302
           |||    |||:::||     ||  :::: :::|||:::|||               |||
Db    71 AlaProLeuGluLeuArgAspCysIleLysLysIleAlaValIleTyrGlyAsnProLysCys 90

Qy   303 GATGTC---TTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAGCAGGCGCTTTCAGC 359
           |||||     |||::: ::  ||    |||:||
Db    91 AspIleHisLeuLysAspGlyGlnGlyTyrTrpSerTyrIleValGluArgProSerAlaProGlu 110

Qy   360 AAT---TGCTACCCATATGAACATCCCTGACTATGCAGTCGCTCCGGTCCATTGTAGCATCC 416
           |||     ||     ::|| ::||||  ||   ::  :|||
Db   111 GlyMetCysTyrProGlySerIleGluValIleGluLysLeuAsnGluLeuArgPheValPheSer 130

Qy   417 TCAGAAACAATTAGAA---TTCACAGCAGAGGGATTCACATGGACAGGTGTGTCACTCAAAAC 473
           :::::::          ::
Db   131 AlaAlaSerTyrLysArgLeuProLeuGlnPheAspTyrSerArgTrpAsnValThrArg 150

Qy   474 GGAAGAAGTGGAGCCTGCAAAAGGGGATCA--GCCGATAGTTTCTTAGCCGACTGAAT 530
           :::       ||| :::||||       :::  ||||
Db   151 GlyTyrThrSerLysAlaCysAsnAlaSerThrGlyGlyGlnSerPheTyrArgSerIleAsn 170

Qy   531 TGGCTAACA---AAATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAAT 587
           |||||||||       :::::||     |||
Db   171 TrpLeuThrLysLysProAspThrTyrAspPheAsnGluGlyThrTyrValAsnAsn 190

Qy   588 AAAAATTCGACAAACTATCATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAG 647
           ::::|||||||: :||  ||| ||| :::
Db   191 GluAspGlyAspIleIlePheLeuTrpIleHisHisProProAspThrLysGluGln 210

Qy   648 ACAGAATTGTACATCCAAGATCAGGACGTAACAGTCTCAACAAAAGAAGTCAACAA 707
           |||  |||||       :::   ::||  |||
Db   211 ThrThrLeuTyrLysAlaAlaAsnThrLeuThrAsnThrIleAsnArg 230

Qy   708 ACGATAGTCCCTAATATCGGATCTAGACGGTGGGTTAGGGTCAATCAGGCAGGATAAGC 767
           ||||||    |||||   ||||
Db   231 AsnPheGlnProAsnIleGlyProLeuValArgGlyGlnGlnGlyArgMetAsp 250

Qy   768 ATATACTGGACCATTGTAAAACCTGAAGAATCCTAATGATAAAACAGTAATGGCAACTTA 827
           |||:::||||||      ||||||  :||:   ::::||
Db   251 TyrTyrTyrTrpGlyIleLeuLysArgGlyValGlyThrGluThrLeuLysLeuIleArgThrAsnGlyAsnLeu 270
```

```
Qy   828 GTTGCACCGGCGGGGATATTTAAATTGAAACAGGGAAAAGCTCT-------GTAATG 878
           ::||||||||      |||  :::  ||||||||||::::|||
Db   271 IleAlaProGluPheGlyTyrLeuLeuLys---GlyGluSerHisGlyArgIleIleGln 289

Qy   879 AGATCAGATGCACCCATAGATCATTTGTGTGTCTGAATGATTACCAAATGGAAGCATC 938
           |||||          ||||:::  :||||||||  |||  :::
Db   290 AsnGluAspIleProIleGlyAsnCysAsnThrLysCysGlnThrTyrAlaGlyAlaIle 309

Qy   939 CCCAACGACAAACCATTCAAATGTGAACAAGTTACATATGGAAAATGCCCAAGTAT 998
           :::         ||||||||||||::       :::||||||||||:::|||||
Db   310 AsnSerSerLysProPheGlnAsnAlaSerArgHisTyrMetGlyCysProLysTyr 329

Qy   999 ATCAGGCAAAACAACTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAAAAGACAAATC 1058
           :::::::  :::|||::||| :||||:||
Db   330 ValIleLysLysAlaSerLeuArgLeuAlaValGlyLeuArgAsnThrProSerValGluPro 349

Qy  1059 AGA 1061
           |||
Db   350 Arg 350
```

```
RESULT 9
US-10-381-530-12
; Sequence 12, Application US/10381530
; Publication No. US2004013701A1
; GENERAL INFORMATION:
;  APPLICANT: KATINGER, Hermann
;  APPLICANT: EGOROV, Andre
;  APPLICANT: FERKO, Boris
;  APPLICANT: ROMANOVA, Julia
;  APPLICANT: KATINGER, Dietmar
;  TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE
;  FILE REFERENCE: P/167-134
;  CURRENT APPLICATION NUMBER: US/10/381,530
;  CURRENT FILING DATE:   2003-11-24
;  PRIOR APPLICATION NUMBER: PCT/EP01/11087
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: 00120896.6
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;  LENGTH: 562
;  TYPE: PRT
;  ORGANISM: Influenza virus A/Singapore/1/57/ca
US-10-381-530-12

Alignment Scores:
Pred. No.:            1.63e-42        Length:              562
Score:               517.00          Matches:             108
Percent Similarity:  52.01%          Conservative:         60
Best Local Similarity: 33.44%        Mismatches:          149
Query Match:         27.04%          Indels:                6
DB:                                  Gaps:                  5

US-10-826-929A-1 (1-1061) x US-10-381-530-12 (1-562)

Qy   111 TTATGTCTGGACACCATGCAGTAGCAGTAGCAAATGGAACATTGGTAAAACAATAACTGATGAC 170
           ::|||:::||:||:||    :::         |||
Db    18 IleCysIleGlyTyrHisAlaAsnAsnSerThrGluLysValAspThrIleLeuGluGln 37

Qy   171 CAAATTGAGGTGACAAAATGCTACTAGTTCAGAGCATTTCAGAGCATTTCAGAGCATTTCAGGAAAATATGC 230
           :::        ||| ||:::||||:::|||::: |||:::
Db    38 AsnValThrValThrHisValAlaLysAspIleLeuGluLysLysThrHisAsnGlyLysLeuCys 57

Qy   231 AAC---AACTCATATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCAATGCTA 287
           |||    :::||  :::|| ::       ||  :::|||
Db    58 LysLeuAsnGlyIleProLeuGluLeuGlyAspCysSerIleAlaGlyTrpLeuLeu 77

Qy   288 GGAGACCCCCACTGTGAT---GTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGA 344
           ||:::||||      ::::
Db    78 GlyAsnProGluCysAspSerArgLeuLeuSerValProGluTrpSerTyrIleMetGluLys 97
```

Db   54 ThrAsnValProArgIleCysSerLysArgSerGlyLysArgThrValAspLeuGlyGlnCysGly 73
Qy 270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGATGTCTTCCAGTATGATGGAATTGGGAC   329

Db   74 LeuLeuGlyThrIleThrGlyProProGlnCysAspGlnPheLeuGluPheSerAlaAsp   93
Qy 330 CTCTTCATAGAAAGGAGAGCAGCGGCTTCAGCAATTGCTACCCATATGACATCCTGACTAT   389

Db   94 LeuIleIleGluArgArgGluGlyGlySerAspValCysTyrProGlyLysPheValAsnGlu   113
Qy 390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGAGAGGGGATTC   449

Db 114 GluAlaLeuArgGlnIleLeuArgGluSerGlyGlyIleAspLysGluAlaMetGlyPhe   133
Qy 450 ACATGACACAGGTGTCACTCAAAAGCGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT   509

Db 134 ThrTyrSerGlyIleArgThrAsnGlyThrThrSerAlaCysArgArg------SerGlySer 152
Qy 510 AGTTTCTTAGCCGACTGAATTGGCTAACAAAATCTGGAAAC-------TCTTACCCCACA   563

Db 153 SerPheTyrAlaGluMetLysTrpLeuLeuSerAsnThrAspAsnAlaAlaPheProGln   172
Qy 564 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGCGGCCACTTGGGGATGAGGAATATCAT   623

Db 173 MetThrLysSerTyrLysAsnThrArgLysAspProAlaLeuIleIleTrpGlyIleHis   192
Qy 624 CACCCGAGCTCAAACCAACAGCAGATTGTACATCCCAAGAATCAGGACGAGTAACA   683

Db 193 HisSerGlySerThrThrGluGlnThrLysLeuTyrGlySerGlyAsnLysLeuIleThr   212
Qy 684 GTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTAATATCGGATCCAGACCTGTGGGT   743

Db 213 ValGlySerSerAsnTyrGlnGlnSerPheValProSerProGlyAlaArgProGlnVal   232
Qy 744 AGGGGTCAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTA   803

Db 233 AsnGlyGlnSerGlyArgIleAspPheHisTrpLeuMetLeuAsnProAsnAspThrVal   252
Qy 804 ATGATAAACAGTAATGGCAACTTAGTTGCACCG---CGGGGATATTTAAATTGAAAACA   860

Db 253 ThrPheSerPheAsnGlyAlaPheIleAlaProAspArgAlaSerPhe-----LeuArg   270
Qy 861 GGGAAAAGCTCTGTAATGGAACTCAGGATCAGATGCACCCATAGACATT--TGTGTGTCTGAATGT 917

Db 271 GlyLysSerMetGlyIleGlnSerGlyValGlnValAspAlaAsnCysGluGlyAspCys   290
Qy 918 ATTACCACCAAATGAAGCATCCCAAGCACAAACCATTCAAAATGTGAACAAAGTTACA   977

Db 291 TyrHisSerGlyGlyThrIleIleSerAsnLeuProPheGlnAsnIleAsnSerArgAla   310
Qy 978 TATGGAAAATGCCCCAAGTATATCAGGCAAAAACTTAAAGCTCGGCCACTGGGATGAGG   1037

Db 311 ValGlyLysCysProArgTyrValLysGlnGluSerLeuLeuLeuAlaThrGlyMetLys   330
Qy 1038 AATATACCAGAA   1049

Db 331 AsnValProGlu   334

RESULT 7

Alignment Scores:

Pred. No.:	2.63e-55	Length:	564
Score:	645.00	Matches:	132
Percent Similarity:	57.56%	Conservative:	66
Best Local Similarity:	38.37%	Mismatches:	132
Query Match:	33.73%	Indels:	14
DB:	13	Gaps:	7

US-10-826-929A-1 (1-1061) x US-10-099-619-2 (1-564)

Qy 690 ACAAAAGAAGTCAACAAACGATAGTCCCTAATATCGGATCCAGACCTGGGTTAGGGGT   749
Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProArgValArgGly   240

Qy 750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA   809
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle   260

Qy 810 AACAGTAATGGCAACTTAGTTGCACCGCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC 869
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgArgGlyTyrPheLysLeuLysThrGlyLysSer 280

Qy 870 TCTGTAATGGAACTCAGGATCAGACATTTGTGTGTCTGAATGTATTACACCAAAT   929
Db 281 SerValMetArgSerArgAspGlnThrPheCysValCysSerGluCysIleThrProAsn   300

Qy 930 GGAAGCATCCCAACGACAAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC   989
Db 301 GlySerIleProThrAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGCGGCCACTTGGGGATGAGGAATATACCAGAA 1049
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuLeuAlaThrGlyMetArgAsnValProGlu 340

Qy 1050 AAGCAAATCAGA   1061
Db 341 LysGlnIleArg 344

RESULT 8

Qy   30 ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCACC   89
Db   1 MetAsnThrGlnIleLeuValPheAlaLeuValAlaIleIle--------ProThr   16

Qy   90 AGTGGAAACAACACAGCCACCATTATGTCTGGACACCAGTCAGTAGCAAATGGAACATTG   149
Db   17 SerAlaAspLys--------IleCysLeuGlyHisHisAlaValSerAsnGlyThrLys   33

Qy 150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC   209
Db   34 ValAsnThrLeuThrGlyValGluValGluValAlaThrGluThrValGluArg   53

Qy 210 ATTTCAATAGGGAAAATAATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269

```
; GENERAL INFORMATION:
;  APPLICANT: Dowling, Patricia W.
;  APPLICANT: Youngner, Julius S.
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/734,373
;  CURRENT FILING DATE: 2003-12-12
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 8
;  LENGTH: 565
;  TYPE: PRT
;  ORGANISM: Equine influenza virus H3N8
US-10-734-373-8
```

```
Alignment Scores:
Pred. No.:
Score:                   1.98e-169    1787.00
Percent Similarity:      99.42%                  Length:        565
Best Local Similarity:   96.80%                  Matches:       333
Query Match:             93.46%                  Conservative:  9
                         16                      Mismatches:    2
DB:                                              Indels:        0
                                                 Gaps:          0
```

```
US-10-826-929A-1 (1-1061) x US-10-734-373-8 (1-565)

Qy    30 ATGAAGACAACACCATTATTTGATACTGACCCATTGGGTCTACAGTCAAAACCCACC      89
            ||||||||||||||||||||||||||||||||||||||
Db     1 MetLysThrThrIleIleLeuIleLeuIleProLeuThrHisTrpValTyrSerGlnAsnProThr  20

Qy    90 AGTGGAAACAACAGCCACCATTATGTCTCGGGACACCAGTAGCAAATGGAACATTG     149
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu         40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGTGACAAATGTACTAGTTCAGAGC       209
Db    41 ValLysThrIleThrAspAspGlnIleGluThrAsnAlaThrGluLeuValGlnSer           60

Qy   210 ATTTCAATAGGAAAATATGCAACAACTCATATAAAGTTCTAGATGAAGAAATTGCACA   269
            ||||||||||||:::
Db    61 IleSerIleGlyLysTyrAlaThrThrHisSerSerTyrArgValLeuAspGlyAsnCysThr      80

Qy   270 TTAATAGATGCAATGCTAGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC   329
Db    81 LeuIleAspAlaMetLeuGluThrProHisCysSerAspValPheGlnTyrGluAsnTrpAsp     100

Qy   330 CTCTTCATAGAAAGAAGAGCAGCGCTTTCAGCAATTGCTACCCATAATGACATCCCTGACTAT 389
Db   101 LeuPheIleGluArgSerSerAlaPheSerSerTyrCysTyrProTyrAspIleProAspTyr    120

Qy   390 GCATCGCTCCGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC  449
Db   121 AlaSerLeuArgSerIleValAlaSerGlyThrLeuGluPheThrAlaGluGlyPhe          140

Qy   450 ACATGGACAGGTGTCACTCAAAACGGAAGAGAGTGAGCCTGCAAAAGGGGATTCAGCCGAT 509
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp       160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAAACTCTTACCCCACATTGAAT 569
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn       180

Qy   570 GTGACAATGCCTAACATAAAAATTCGACAACATACATCTGGGGATTCATCACCCG      629
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro       200

Qy   630 AGCTCAAACAACAACAGCACAGAGAATTGTACATCCAAGAATGTATGCAGGAGTAACAGTCTCA 689
            ::::::|||
Db   201 SerSerAsnLysGluGlnThrIleTyrIleGlnGluSerGlyArgValThrValSer          220
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```
RESULT 6
US-10-734-373-8
; Sequence 8, Application US/10734373
; Publication NO. US20040137015A1

Qy    90 AGTGGAAACAACAGCCACCATTATGTCTCTGGGACACCAGTAGCAAATGGAACATTG    149
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu         40

Qy   150 GTAAAAACAATAATATGCAACACTCATATAAAGTTCTAGATGGAGAAATTGCACA      209
            ||||||||||:::
Db    41 ValLysThrIleThrAspAspSerTyrArgValLeuAspGlyAsnCysThr                 60

Qy   210 ATTTCAATAGGGAAATATGCAACAACTCATATAAAGTTCTAGATGAAGAAATTGGGAC   269
            |||||||||:::
Db    61 IleSerIleGlyLysTyrAlaThrThrHisSerSerTyrArgValLeuAspGluAsnCysThr     80

Qy   270 TTAATAGATGCAATGCTAGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC   329
Db    81 LeuIleAspAlaMetLeuGluThrProHisCysSerAspValPheGlnTyrGluAsnTrpAsp    100

Qy   330 CTCTTCATAGAAAGAAGAGCAGCGCTTTCAGCAATTGCTACCCATAATGACATCCCTGACTAT 389
Db   101 LeuPheIleGluArgSerSerAlaPheSerSerTyrCysTyrProTyrAspIleProAspTyr    120

Qy   390 GCATCGCTCCGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC  449
            |||:::
Db   121 AlaSerLeuArgSerIleValAlaSerGlyThrLeuGluPheThrAlaGluGlyPhe          140

Qy   450 ACATGGACAGGTGTCACTCAAAACGGAAGAGGGGGATCAGCCGAT               509
            |||||||||||||:::
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgGlySerArgGlySerAlaAsp               160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAAACTCTTACCCCACATTGAAT 569
            ||||||||||||:::
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn       180

Qy   570 GTGACAATGCCTAACATAAAAATTCGACAACATACATCTGGGGATTCATCACCCG      629
            |||||||||:::
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro       200

Qy   630 GTGACATGCAATGCCTAACATACTATACTATATGCAACAATAATTTCGACAAATCCG     689
Db   181 ValThrMetProAsnPheAspAsnLysLeuTyrIleTrpGlyIleHisHisPro             200

Qy   630 AGCTCAAACAACAACAGCCAGAGAATTGTACATCCAAGAATGTATGCAGGAGTAACAGTCTCA 689
            :::::|||
Db   201 SerSerAsnLysGluGlnThrIleTyrIleGlnGluSerGlyArgValThrValSer          220

Qy   690 ACAAAAAGAAGTCAACAAACAGATATCCCTAATATCTGGGATCGGTAGTAGAGCCGTGGGGT 749
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProArgValArgGly      240

Qy   750 CAATCAGGCAGGATAAGCATTTGTGTAAACCTGGAGATATCCTAATGATA         809
Db   241 GlnSerGlyArgIleSerIleSerTyrTyrIleValIleValIleValProGlyIleLeuMetIle  260

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC   869
Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer       280

Qy   870 TCTGTAATGAGATCAGATGCCCATGCCCATGCATTTGTGTCTCAATGAATGTATTTCTGATGATA 929
Db   281 SerValMetArgSerAspAlaProIleGlyAspCysAsnSerGluCysIleThrProAsn      300

Qy   930 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAAAATGC 989
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnAsnValThrTyrGlyLysCys      320

Qy   990 CCCAAGTATATCAGGACAAAACACTTTAAAGCTGGGCCACTGGCATGAGGAGATATACCAGAA 1049
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Db   321 ProLysTyrIleArgGlnAsnThrLeuArgLeuAlaThrGlyMetArgAsnValProGlu      340

Qy  1050 AAGCAAATCAGA      1061
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Db   341 LysGlnIleArg      344
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Db   341 LysGlnIleArg 344

RESULT 4
US-10-065-133A-8
; Sequence 8, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
;   APPLICANT: Dowling, Patricia W.
;   APPLICANT: Youngner, Julius S.
;   TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;   FILE REFERENCE: EQ-1-C2-1
;   CURRENT APPLICATION NUMBER: US/10/065,133A
;   CURRENT FILING DATE: 2002-12-10
;   PRIOR APPLICATION NUMBER: PCT/US99/18583
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 09/133,921
;   PRIOR FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 108
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 565
;   TYPE: PRT
;   ORGANISM: Equine influenza virus H3N8
US-10-065-133A-8

Alignment Scores:
Pred. No.:              1.98e-169       Length:          565
Score:                  1787.00         Matches:         333
Percent Similarity:     99.42%          Conservative:    9
Best Local Similarity:  96.80%          Mismatches:      2
Query Match:            93.46%          Indels:          0
DB:                                     Gaps:            0

US-10-826-929A-1 (1-1061) x US-10-065-133A-8 (1-565)

Qy    30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCACC    89
         ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db     1 MetLysThrThrIleIleLeuIleProLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy    90 AGTGGAAACAACAGCCACATTATGTCTGGGACACCATGTCAGTAGCAAATGGAACATTG   149
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACACAAATGCTACTGAATTAGTTCAGAGC   209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy   210 ATTTCAATAGGGGAAAATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA   269
         ||||||||||||||||||||||||  |||::|||  |||||||||||||||||||||||
Db    61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr   80

Qy   270 TTAATAGATGCAAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC   329
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyTyrLeuAspProHisCysAsnGlnTyrGluAsnTrpAsp   100

Qy   330 CTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT   389
         |||||||||||||||||||||||||||  |||::|||||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyrProTyrAspIleProAspTyr   120

Qy   390 GCAATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC   449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe   140

Qy   450 ACATGGACAGGTGTCACTCAAAACGGAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT   509
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp   160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT   569
         ||||||||||||||||::|||||||||||||||||||||||||||||||||||||||||
Db   161 SerPheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn    180

Qy   570 GTGACAATGCCTAACAATAAACAATAAAAATTTCGACAAACTATACATCTCGGGGGATTCATCACCCG   629
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Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLysTyrIleIleTrpGlyIleHisHisPro   200

Qy   630 AGTCAAACCAACACGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA   689
         ||||||||||||||||::::|||||||||||||||||||||||||||||||||||||||
Db   201 SerSerAsnLysGluGlnLnThrLysTyrIleGluTyrIleGluSerGlyArgValThrValSer   220

Qy   690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATGGATCTCGGAATCGGTAGGGGT   749
         |||||||||||::|||||||||||||||||||||||::||||||||||||||||||
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgArgProArgValArgGly   240

Qy   750 CAATCAGGCAGGATAAGCATCATATGCGACCATTGGACCATTGTAAAACCTGGAGATAATCCTAATGATA   809
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GlnSerGlyArgIleSerIleTyrTyrTThrIleTyrThrIleValLysProGlyAspIleLeuMetIle   260

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTTAAATTGAAAACAGGGAAAAGC   869
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnSerSerAsnGlyAsnLeuValAlaProArgAspIleLeuLysLysThrGlyLysSer   280

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGTATTACCACAAAT   929
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn   300

Qy   930 GGAAGCATCCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC   989
         ||||||||||||||||||||||||||||||||||||||||||||||||::|||||||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys   320

Qy   990 CCCAAGTATATCAGGCAAAACACTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA  1049
         |||||||||||||||||||||||||||||||||::|||||||||||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu   340

Qy  1050 AAGCAAATCAGA  1061
         ||||||||||||
Db   341 LysGlnIleArg  344

RESULT 5
US-10-434-811A-8
; Sequence 8, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;   APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;   APPLICANT: Education
;   APPLICANT: Dowling, Patricia W.
;   APPLICANT: Youngner, Julius S.
;   TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;   FILE REFERENCE: EQ-1-C1-PUS-1
;   CURRENT APPLICATION NUMBER: US/10/434,811A
;   CURRENT FILING DATE: 2003-05-08
;   PRIOR APPLICATION NUMBER: PCT/US99/18583
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 09/133,921
;   PRIOR FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 565
;   TYPE: PRT
;   ORGANISM: Equine influenza virus H3N8
US-10-434-811A-8

Alignment Scores:
Pred. No.:              1.98e-169       Length:          565
Score:                  1787.00         Matches:         333
Percent Similarity:     99.42%          Conservative:    9
Best Local Similarity:  96.80%          Mismatches:      2
Query Match:            93.46%          Indels:          0
DB:                                     Gaps:            0

US-10-826-929A-1 (1-1061) x US-10-434-811A-8 (1-565)

Qy    30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCACC    89
         ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db     1 MetLysThrThrIleIleLeuIleProLeuThrHisTrpValTyrSerGlnAsnProThr   20
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DB:                              16          Gaps:           0

US-10-826-929A-1 (1-1061) x US-10-734-373-11 (1-565)

Qy     30 ATGAAGACAACCATTATTGATACTACTGACCTCTTACCCCACATTGAAT  89
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr  20

Qy     90 AGTGGAAACACAGCCACCATTATGTCTGGGACATCTGGGGATTCATCACCCCG  149
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaValAlaAsnGlyThrLeu  40

Qy    150 GTAAAAACAATAACTGATGACCAAATTGAGTGACAAATGCTACTGAATTAGTTCAGAGC  209
          ||||||||||||::||:||||||||||||||||||||||||||||||||
Db     41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer  60

Qy    210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA  269
          ||||||||||||||||||||||||||||||:||||||||||||||:::||||||||
Db     61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr  80

Qy    270 TTAATAGGACCAATGCTAGGAGCACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC  329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp  100

Qy    330 CTCTTCATAGAAAGAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTACT  389
          ||||||||||||||||||||||||||::||||||||||||||||||||
Db    101 LeuPheIleGluArgSerAlaPheSerAlaIleProIleProTyrAspTyr  120

Qy    390 GCATCGCTCCGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCGAGGGATTC  449
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe  140

Qy    450 ACATGACAGGTGTCACTCAAAACGGAAGAGTGGAGCCTGCAAAAGGGGATCAGCCGAT  509
          ||||||||||||||||||||||||||||||||::::|||||||||||||||
Db    141 ThrTrpThrGlyValThrGlnAsnGlyArgSerCysLysArgGluSerAlaAsp  160

Qy    510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATTGGAAACTCTTACCCCACATTGAAT  569
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 SerPhePheSerArgLeuAsnTrpLeuThrGluThrProHisLeuAsn  180

Qy    570 GTGACAATGCCTAACAATAAAAATTCGACAAACATACATCTGGGGGATCATCACCCG  629
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ValThrMetProAsnAsnLysAsnPheAspLysTyrIleLeuTrpGlyIleHisHisPro  200

Qy    630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGACTAACAGTCTCA  689
          |||||||:::::||||||||||||||||||||||||||||||||||:||
Db    201 SerSerAsnLysGlnGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer  220

Qy    690 ACAAAAGAAGTCAACAACGATAGTCCCTAATATCGGATATTGGCCAGTCTAGACCGTGGTTAGGGGT  749
          ||||||||||||||||||||:::||||||||||||||||||||||||||
Db    221 ThrLysArgSerGlnAsnThrIleIleProAsnIleGlySerArgProTrpValArgGly  240

Qy    750 CAATCAGGCCAGATAAGCAATATACTGACCATTGTAAAACTGGAGATATCCTAATGATA  809
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuThrIle  260

Qy    810 AACAGTAATGCGAACTTAGTTGCACCGCGGGATATTTAAATTGAAACAGGAGAAAAGC  869
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer  280

Qy    870 TCTGTAATGAGATCAGATGCACCCCATAGACATTTGTCTGTCGAAATGTATTACCACCAAAT  929
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluThrProAsn  300

Qy    930 GGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTACATATGGAAAATGC  989
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Db    301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys  320

Qy    990 CCCAAGTATATCAGGCAAAACCTTTAAAGCTGGCCACTGGGATGACGAAATACCAGAA  1049
          |||||||||||||||||||||||||||||:::||||||||||||||||||
Db    321 ProLysTyrIleArgGlnAsnThrLeuLysAlaGlyHisTrpLeuAlaThrGlyMetArgAsnValProGlu  340

Qy   1050 AAGCAAATCAGA  1061
          ||||
Db    341 LysGlnIleArg  344
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RESULT 3
US-10-734-373-11
; Sequence 11, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-11
                     LysGlnIleArg  344

Alignment Scores:
Pred. No.:                          Length:            565
Score:          3.95e-170           Matches:           333
                1794.00             Conservative:        9
Percent Similarity:    99.42%       Mismatches:          2
Best Local Similarity: 96.80%       Indels:              0
Query Match:           93.83%
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Alignment Scores:
Pred. No.:   3.95e-170   Length: 565
Score: 1794.00   Matches: 333
Percent Similarity: 99.42%   Conservative: 9
Best Local Similarity: 96.80%   Mismatches: 2
Query Match: 93.83%   Indels: 0
DB: Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-065-133A-11 (1-565)

Qy   30 ATGAGAACAACCATTATTTTGATACTACTGGGTCTCACAGTCAAAACCCACC   89
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCAGTAGCAAATGGAACATTG   149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACTCACTGAATTAGTTCAGAGC   209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy   210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA   269
          |||||||||||||||||||||||||||::|||||||||||||||||||||||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr   80

Qy   270 TTAATAGATGCAATGCTAGGAGAGCACCCCACTGTGATGTCTCCAGTATGAGAATTGGGAC   329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyGluHisProHisCysAsnGlyArgLeuAspGlyArgAsnTrpAsnTrpAsp   100

Qy   330 CTCTTCATAGAAGAAGCAGCGCTTCAGCAATTGCTACCACCATATGACATCCCTGACTAT   389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuPheIleGluGluAlaAlaLeuGlnArgSerAlaPheSerSerCysTyrProTyrAspIleProAspTyr   120

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGACATTAGAAATCCACAGCGAGGGGATTC   449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGluPhe   140

Qy   450 ACATGGACAGGTGTCACTCAAAAACGGAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT   509
          ||||||||||::::|||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGluSerAlaAsp   160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAAATCTGGAAACTCTTACCCCACATTGAAT   569
          ||||||||||||||||::::||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn   180

Qy   570 GTGACAATGCCTTAACAATAAAAATTCGACAAACTATACATCTGGGAGATTCATCACCCG   629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnLysTyrIleLeuTyrIleTrpGlyValHisHisPro   200

Qy   630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA   689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer   220

Qy   690 ACAAAAAGAAGTCAACAACGATAGTCCCTAATATCGGATCGGGGGTGGGGTTAGGGGGT   749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 ThrLysArgSerGlnGlnThrIleValProAsnIleGlySerArgProValArgGly   240

Qy   750 CAATCAGGCAGGATAAGCCATGGACCATTGTAAAACCTGAAGATATCCTAATGATA   809
          |||||||||||||||||||||||||||||||||:::||||||||||||||||
Db   241 GlnSerGlyArgIleSerHisGlyTyrTyrProGlyThrIleValLysProGluLeuThrIle   260

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTTAAATGAAAACAGGGAAAAGC   869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGlyLysSer   280

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGTATTACCAAAT   929
          |||||||||||||||||||||||||||||::||||||||||||||||||||
Db   281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn   300

Qy   930 GGAAGCATCCCAACGACCCCCAACCATTTCAAAATGTGAACAAAGTTACATGGGAAAATGC   989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys   320

Qy   990 CCCAAGTATATCACGGCAAAACACTTAAAGCTGGATGAGGAATATCACCAGAA   1049
          ||||||||||||||||||||||||||||||::::|||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAspGluGluTyrHisGlnGlu   340

Qy 1050 AAGCAAATCAGA   1061
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Db   341 LysGlnIleArg   344

RESULT 2
US-10-434-811A-11
; Sequence 11, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
;   APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;   APPLICANT: Education
;   APPLICANT: Dowling, Patricia W.
;   APPLICANT: Youngner, Julius S.
;   TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;   FILE REFERENCE: EQ-1-C1-PUS-1
;   CURRENT APPLICATION NUMBER: US/10/434,811A
;   CURRENT FILING DATE: 2003-05-08
;   PRIOR APPLICATION NUMBER: PCT/US99/18583
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 09/133,921
;   PRIOR FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 565
;   TYPE: PRT
;   ORGANISM: Equine influenza virus H3N8
US-10-434-811A-11

Alignment Scores:
Pred. No.:   3.95e-170   Length: 565
Score: 1794.00   Matches: 333
Percent Similarity: 99.42%   Conservative: 9
Best Local Similarity: 96.80%   Mismatches: 2
Query Match: 93.83%   Indels: 0
DB: Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-434-811A-11 (1-565)

Qy   30 ATGAGAACAACCATTATTTTGATACTACTGGGTCTCACAGTCAAAACCCACC   89
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCAGTAGCAAATGGAACATTG   149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACTCACTGAATTAGTTCAGAGC   209
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Qy   210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA   269
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 27, 2005, 18:32:14 ; Search time 157.5 Seconds
(without alignments)
4419.749 Million cell updates/sec

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Perfect score: 1912
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Searched: 1185339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 2770678

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

Result Query

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	1794	93.8	565	15	US-10-434-811A-11	Sequence 11, Appl
3	1794	93.8	565	16	US-10-734-373-11	Sequence 11, Appl
4	1787	93.5	565	14	US-10-065-133A-8	Sequence 8, Appli
5	1787	93.5	565	15	US-10-434-811A-8	Sequence 8, Appli
6	1787	93.5	565	16	US-10-734-373-8	Sequence 8, Appli
7	645	33.7	564	13	US-10-099-619-2	Sequence 2, Appli
8	536.5	28.1	412	14	US-10-224-999A-3466	Sequence 3466, Ap
9	517	27.0	562	16	US-10-381-530-12	Sequence 12, Appl
10	393	20.6	347	9	US-09-918-568-58	Sequence 58, Appl
11	225	11.8	47	14	US-10-105-232-283	Sequence 283, App
12	225	11.8	47	14	US-10-189-437-270	Sequence 270, App
13	222	11.6	584	16	US-10-381-530-30	Sequence 30, Appl
14	205	10.7	346	15	US-10-676-909-90	Sequence 90, Appl
15	184	9.6	39	14	US-10-105-232-284	Sequence 284, App
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17	177	9.3	348	9	US-09-918-568-50	Sequence 50, Appl
18	168	8.8	34	14	US-10-105-232-280	Sequence 280, App
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24	122	6.4	25	14	US-10-351-641-1063	Sequence 1063, Ap
25	118	6.2	24	13	US-10-044-034-11	Sequence 11, Appl
26	111.5	5.8	502	15	US-10-333-002-16	Sequence 16, Appl
27	109	5.7	23	13	US-10-044-034-3	Sequence 3, Appli
28	109	5.7	23	17	US-10-687-711-25	Sequence 25, Appl
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43	97.5	5.1	1180	14	US-10-193-764-61	Sequence 61, Appl
44	97.5	5.1	1188	14	US-10-193-764-59	Sequence 59, Appl
45	97	5.1	1041	9	US-09-042-488B-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-065-133A-11
; Sequence 11, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 11
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-11

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              COUNTRY: USA
                  ZIP: 30309-3450
COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/453,848
          FILING DATE: 30-MAY-1995
       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: 08/120,607
          FILING DATE: 13-SEPT-1993
       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                 NAME: Pabst, Patrea L.
  REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MGS101CIP
TELECOMMUNICATION INFORMATION:
            TELEPHONE: (404)-873-8794
              TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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         HYPOTHETICAL: NO
           ANTI-SENSE: NO
        FRAGMENT TYPE: N-terminal
      ORIGINAL SOURCE:
             ORGANISM: Influenza virus
    INDIVIDUAL ISOLATE: A/Johannesburg/33/94 rHA
FEATURE:
             NAME/KEY: AcNPV 61K protein signal sequence
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             LOCATION: 19 to 569
US-08-453-848-21
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US-10-826-929A-1 (1-1061) x US-08-453-848-21 (1-571)

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Search completed: February 27, 2005, 18:35:14
Job time : 50 secs

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;      CORRESPONDENCE ADDRESS:
;        ADDRESSEE:  Patrea L. Pabst
;        STREET:  2800 One Atlantic Center
;        STREET:  1201 West Peachtree Street
;        CITY:  Atlanta
;        STATE:  GA
;        COUNTRY:  USA
;        ZIP:  30309-3450
;      COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  PC-DOS/MS-DOS
;        SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;        FILING DATE:
;        CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US/08/453,848
;        FILING DATE:  30-MAY-1995
;        APPLICATION NUMBER:  08/120,607
;        FILING DATE:  13-SEPT-1993
;      ATTORNEY/AGENT INFORMATION:
;        NAME:  Pabst, Patrea L.
;        REGISTRATION NUMBER:  31,284
;        REFERENCE/DOCKET NUMBER:  MGS101CIP
;      TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  (404)-873-8794
;        TELEFAX:  (404)-873-8795
; INFORMATION FOR SEQ ID NO:  15:
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;      FRAGMENT TYPE:  N-terminal
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;        ORGANISM:  Influenza virus
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Db     272  LeuIleAlaProArgGlyTyrPheLysIleArgAsnGlyLysSerSerIleMetArgSer  291

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Qy     945  GACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGG  1004
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Db     312  AspLysProPheGlnAsnValAsnArgIleThrTyrGlyAlaCysProArgTyrValLys  331

Qy    1005  CAAAACACTTTAAAGCTGCCACTGGGATGGAGGAGAATATACCAGAAAAGCAAATCAGA  1061
            |||||||||||||||||:::|||          ||
Db     332  GlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGluLysGlnThrArg  350
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;       APPLICANT:  Wilkinson, Bethanie Eident
;       APPLICANT:  Voznesensky, Andrei I.
;       APPLICANT:  Hackett, Craig Stanway
;       TITLE OF INVENTION:  A METHOD FOR PRODUCING INFLUENZA
;       TITLE OF INVENTION:  HEMAGGLUTININ MULTIVALENT VACCINES
;       NUMBER OF SEQUENCES:  31
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  Patrea L. Pabst
;         STREET:  2800 One Atlantic Center
;         STREET:  1201 West Peachtree Street
;         CITY:  Atlanta
;         STATE:  GA
;         COUNTRY:  USA
;         ZIP:  30309-3450
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE:  Floppy disk
;         COMPUTER:  IBM PC compatible
;         OPERATING SYSTEM:  PC-DOS/MS-DOS
;         SOFTWARE:  PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER:  US/08/453,848
;         FILING DATE:  30-MAY-1995
;         CLASSIFICATION:  435
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER:  08/120,607
;         FILING DATE:  13-SEPT-1993
;         CLASSIFICATION:  435
;       ATTORNEY/AGENT INFORMATION:
;         NAME:  Pabst, Patrea L.
;         REGISTRATION NUMBER:  31,284
;         REFERENCE/DOCKET NUMBER:  MGS101CIP
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE:  (404)-873-8794
;         TELEFAX:  (404)-873-8795
; INFORMATION FOR SEQ ID NO:  15:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  571 amino acids
;         TYPE:  amino acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
;       MOLECULE TYPE:  peptide
;       HYPOTHETICAL:  NO
;       ANTI-SENSE:  NO
;       FRAGMENT TYPE:  N-terminal
;       ORIGINAL SOURCE:
;         ORGANISM:  Influenza virus
;         INDIVIDUAL ISOLATE:  A/Shandong/9/93 rHA
;       FEATURE:
;         NAME/KEY:  AcNPV 61K protein signal sequence
;         LOCATION:  1 to 18
;       FEATURE:
;         NAME/KEY:  mature rHA
;         LOCATION:  19 to 553
; US-08-453-848-15
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Alignment Scores:
Pred. No.:                  2.02e-139        Length:            571
Score:                      1404.50          Matches:           253
Percent Similarity:         86.73%           Conservative:      41
Best Local Similarity:      74.63%           Mismatches:        44
Query Match:                73.46%           Indels:            1
DB:                         2                Gaps:              1
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US-10-826-929A-1 (1-1061) x US-08-453-848-15 (1-571)

Qy    48  TTGATACTACTGACCCATTGGGTCTCACAGTCAAAAC---CCAACCAGTGGAAACAACACA  104
              |||  ||::::|| :||  ||   |||||  ::: |||  ||:::||||
Db    12  LeuValAlaValSerAsnAlaIleProGlyGlnAspLeuProGlyAsnAspAsnSerThr   31

Qy   105  GCCACCATTATGTCTGGGACCACCATGGCAGTAGCAAATGGAACAATGGTAAAAACAATAACT  164
              ||||||:|| |||  |||  ||  ||||||      ||||||||:|||  :||:|||
Db    32  AlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThrLeuValLysThrIleThr    51
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RESULT 14
US-09-169-027-15
; Sequence 15, Application US/09169027
; Patent No. 6245532
; GENERAL INFORMATION:
;       APPLICANT:  Smith, Gale Eugene
;       APPLICANT:  Volvovitz, Franklin
;       APPLICANT:  Wilkinson, Bethanie Eident
;       APPLICANT:  Voznesensky, Andrei I.
;       APPLICANT:  Hackett, Craig Stanway
;       TITLE OF INVENTION:  A METHOD FOR PRODUCING INFLUENZA
;       TITLE OF INVENTION:  HEMAGGLUTININ MULTIVALENT VACCINES
;       NUMBER OF SEQUENCES:  31
```

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Qy   165  GATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGCATTCAATAGGGAAA   224
              :::||||||||||| |||| |||||||||| |||||||| ||| ||::::
Db    52  AspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSerSerThrGlyArg    71

Qy   225  ATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGTGACCAATG   284
          ||||     |||| :::    ::::||||::||||||| |||||||||||||||:|||||||
Db    72  IleCysGlySerProHisArgIleLeuAspGlyLysAsnCysThrLeuIleAspAlaleu   91

Qy   285  CTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAAGGACCCTTCATAGAAGA   344
          ||||||||||||||||||||| ||:|| :|| |||:||||||||||||||
Db    92  LeuGlyAspProHisCysGlyAspGlyPheGlnAsnLysGluTrpAspLeuVsluArg   111

Qy   345  AGCAGGCGCTTCAGCAATTGCTACCCATATGACATCCCGACTATGCATGGCATGCGGTCC   404
          ||||||| |||||||||||:|||||||:||||||:::||||||||||||||
Db   112  SerLysAlaTyrSerAsnCysTyrProTyrAspValProAspTyrAlaSerLeuArgSer   131

Qy   405  ATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGGTGTC   464
          ||||| |||||||||||| |||| ::|||||||||||||||||||||||
Db   132  LeuValAlaSerSerGlyThrLeuGluPheIleAsnGluAspPheAsnTrpThrGlyVal   151

Qy   465  ACTCAAAACGAAGAAGTGGAGCCTCGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGA   524
          ||:||||| |||||||| ||:|| ||||||||||| :::||||||||||||
Db   152  AlaGlnAspGlyGlySerTyrAlaCysLysLysArgGlySerValAsnSerPheSerArg   171

Qy   525  CTGAATTGGCTAACAAAATCTGGAAACTCTTACCCACCATTGAAATGTGACAAATGCCTAAC   584
          |||||||||||| ||| ||||||||||||||||| ::||||||||||||||
Db   172  LeuAsnTrpLeuHisLysGluTyrLysTyrProAlaLeuAsnValThrMetProAsn   191

Qy   585  AATAAAAATTTCGACAAACATACATCTGGGGATTCATCACCCGAGCTCAAACCAACAG   644
          |||||||||| ||:||||||||||||||||||||||||||||:|||:|||||
Db   192  AsnGlyLysPheAspLysHisLeuTyrIleTrpGlyValHisHisProSerThrAspSerAsp   211

Qy   645  CAGAGAATTGTACATCCAAGAAATCAGGAGGACGAGTAACAGTCTCAACAAAAGAAGTCAA   704
          ||||| |||||||||||||||||||||| ||||||||||| ||||||||||
Db   212  GlnThrSerLeuTyrValArgAlaSerGlyArgValThrValSerThrLysArgSerGln   231

Qy   705  CAAACGATAGTCCCTATATCGGATCCTAGATCAGACCGTGGGTTAGGGTCAATCAGGCAGGATA   764
          |||||||:::| |||||||||| |||||||||||||| |||||||||
Db   232  GlnThrValThrProAsnIleGlySerArgProValArgGlyGlnSerSerArgIle   251

Qy   765  AGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAAC   824
          |||||||||||||||||||||||  |||||||||:::|||||||||||
Db   252  SerIleTyrTrpThrIleValLysProGlyAspIleLeuLeuIleAspSerThrGlyAsn   271

Qy   825  TTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGCTTCTGTAATGAGATCA   884
          ||||||| |||||||||||||||:::|||   ||||||||||||:::||||||
Db   272  LeuIleAlaProArgGlyTyrPheLysIleArgAsnGlyLysSerSerIleMetArgSer   291

Qy   885  GATGCACCCATAGACATTTGTGTCTGGAATGTATTACCACCAAATGGAAGCATCCCCAAC   944
          ||||| |||||||||||||| :|||||||||||||||||||||
Db   292  AspAlaProIleGlyAsnCysAsnSerGluCysIleThrProAsnGlySerIleProAsn   311

Qy   945  GACAAAACCATTTCAAAATGTGAACAAGTTACATATGGAAAATGCCCAAGTATATCAGG   1004
          |||||||||||:::|||||||||||||||||:::|||||
Db   312  AspLysProPheGlnAsnValAsnArgIleThrTyrGlyAlaCysProArgTyrValLys   331

Qy  1005  CAAAACACTTTAAAGCTGGCCACTGGCATCGGATGGAATATACCAGAAAAGCAAATCAGA   1061
          |||||||||||||||||| :::||||||||||||||||||:::||||||||
Db   332  GlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGluLysGlnThrArg   350
```

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; Sequence 7, Application US/09169027
; Patent No. 6245532
; GENERAL INFORMATION:
;   APPLICANT: Smith, Gale Eugene
;   APPLICANT: Volvovitz, Franklin
;   APPLICANT: Wilkinson, Bethanie Eident
;   APPLICANT: Voznesensky, Andrei I.
;   APPLICANT: Hackett, Craig Stanway
;   TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
;   TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Patrea L. Pabst
;     STREET: 2800 One Atlantic Center
;     STREET: 1201 West Peachtree Street
;     CITY: Atlanta
;     STATE: GA
;     COUNTRY: USA
;     ZIP: 30309-3450
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/169,027
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/453,848
;     FILING DATE: 30-MAY-1995
;     APPLICATION NUMBER: 08/120,607
;     FILING DATE: 13-SEPT-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pabst, Patrea L.
;     REGISTRATION NUMBER: 31,284
;     REFERENCE/DOCKET NUMBER: MGS101CIP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (404)-873-8794
;     TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 570 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: N-terminal
;   ORIGINAL SOURCE:
;     ORGANISM: Influenza virus
;     INDIVIDUAL ISOLATE: A/Bejing/32/92 rHA
;   FEATURE:
;     NAME/KEY: AcNPV 61K protein signal sequence
;     LOCATION: 1 to 18
;   FEATURE:
;     NAME/KEY: mature rHA
;     LOCATION: 19 to 552
US-09-169-027-7

US-10-826-929A-1 (1-1061) x US-09-169-027-7 (1-570)

Alignment Scores:
Pred. No.:              3.67e-141    Length:        570
Score:                  1421.00      Matches:       254
Percent Similarity:     87.28%       Conservative:   41
Best Local Similarity:  75.15%       Mismatches:     43
Query Match:            74.32%       Indels:          0
DB:                     3            Gaps:            0

Qy   48 TTGATACTACTGACCCATTGGGTCTACAGTCCAAAACCCACCAGTGGAAACAACACAGCC 107

Db   12 LeuValAlaValSerAsnAlaIleProGlyAspPheProGlyAspAsnSerThrAla 31
Qy  108 ACATTAATGTCTGGAGACACCATGCAGTAGCAGTGCAAATGAACATTGGTAAAACAATAACTGAT 167
Db   32 ThrLeuCysLeuGlyHisHisAlaValProAsnGlyThrLeuValLysThrIleThrAsn 51
Qy  168 GACCAAATTGAGGTGACAAATGCTACTGACTTGAATTAGTTCAGAGCATTCAATAGGAAAAATA 227
Db   52 AspGlnIleGluValThrAsnAlaThrGluLeuValGlnSerSerThrGlyArgIle 71
Qy  228 TGCAACAACTCATATAAAGTTCTAGATGAAGAAATTGCACATTAATAGATGCAATGCTA 287
Db   72 CysAsnSerProHisArgIleLeuAspGlyLysAsnCysThrLeuIleAspAlaLeuLeu 91
Qy  288 GGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGGACCTCTTCATAGAAAGAAGC 347
Db   92 GlyAspProHisCysAspGlyPheGlnAsnLysGluTrpAspLeuPheValGluArgSer 111
Qy  348 AGCGCTTTCAGCAATTGCTACCCATATGACATCCTGACTATGCATCGCTCCGGTCCATT 407
Db  112 LysAlaTyrSerAsnCysTyrProTyrAspValProAspTyrAlaSerLeuArgSerLeu 131
Qy  408 GTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGATTCACATGGACAGGTGTCACT 467
Db  132 ValAlaSerSerGlyThrLeuGluPheIleAsnGluAspPheAsnTrpThrGlyValAla 151
Qy  468 CAAAACGGAGAAGGTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTAGCCGACTG 527
Db  152 GlnAsnGlyGlySerTyrAlaCysLysArgGlySerValAsnSerPhePheSerArgLeu 171
Qy  528 AATTGGCTAACAAAATCTTACCCCACATTGAATGTGACAATGCCTAACAAT 587
Db  172 AsnTrpLeuHisLysSerGluTyrLysTyrProAlaLeuAsnValThrMetProAsnAsn 191
Qy  588 AAAAATTTGACAAACTATACATCTGGGGATTCATCACCCGAGTCAAACCAACAGCAG 647
Db  192 GlyLysPheAspLeuTyrIleTrpGlyValHisHisProSerThrAspArgAspGln 211
Qy  648 ACAGAATTGTACATCCAAGAATCAGGAGCGAGTAACAGTCTCAACAAAAGAAGTCAACAA 707
Db  212 ThrSerLeuTyrValArgAlaSerGlyArgValThrValSerThrLysArgSerGlnGln 231
Qy  708 ACGATAGTCCCTAATATCGGATCTAGACCGTGGTTAGGGTCAATCAGGCAGGATAAGC 767
Db  232 ThrValThrProAsnIleGlySerArgProTrpValArgGlyLeuGlySerArgIleSer 251
Qy  768 ATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTA 827
Db  252 IleTyrTrpThrIleValLysProGlyAspIleLeuLeuIleAsnSerThrGlyAsnLeu 271
Qy  828 GTTGCACCGCGGGATATTTTAAATTGAAAACAGGAAAAGCTCGTAATGAGATCAGAT 887
Db  272 IleAlaProArgGlyTyrPheLysIleArgAsnGlyLysSerSerIleMetArgSerAsp 291
Qy  888 GCACCCATAGACAGCATTTGTGTCTGAAATGTATTACCACAAATGAAGCATCCCCAACGAC 947
Db  292 AlaProIleGlyThrCysSerSerGluCysIleThrProAsnGlySerIleProAsnAsp 311
Qy  948 AAACCATTTCAAAATGAACAAAGTTACATATGAAAAATGCCCCAAGTATATCAGGCAA 1007
Db  312 LysProPheGlnAsnValAsnArgIleThrTyrGlyAlaCysProArgTyrValLysGln 331
Qy 1008 AACACTTTAAAGCTGGCCACTGGGATGAGAATATACCAGAAAAGCAAAATCAGA 1061
Db  332 AsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGluLysGlnThrArg 349

RESULT 13
US-08-453-848-15
; Sequence 15, Application US/08453848
; Patent No. 5858368
; GENERAL INFORMATION:
;   APPLICANT: Smith, Gale Eugene
;   APPLICANT: Volvovitz, Franklin
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Qy   1047 GAAAAGCAAATCAGA 1061
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Db    341 GluLysGlnThrArg 345
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RESULT 11
US-08-453-848-7
; Sequence 7, Application US/08453848
; Patent No. 5858368
; GENERAL INFORMATION:
; APPLICANT: Smith, Gale Eugene
; APPLICANT: Volovitz, Franklin
; APPLICANT: Wilkinson, Bethanie Eident
; APPLICANT: Voznesensky, Andrei I.
; APPLICANT: Hackett, Craig Stanway
; TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
; TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,848
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120,607
; FILING DATE: 13-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MGS101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus
; INDIVIDUAL ISOLATE: A/Bejing/32/92 rHA
; FEATURE:
; NAME/KEY: ACNPV 61K protein signal sequence
; LOCATION: 1 to 18
; FEATURE:
; NAME/KEY: mature rHA
; LOCATION: 19 to 552
US-08-453-848-7

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Alignment Scores:
Pred. No.:        3.67e-141
Score:            1421.00
Percent Similarity:       87.28%          Length:        570
Best Local Similarity:    75.15%          Matches:       254
Query Match:              74.32%          Conservative:   41
                                          Mismatches:     43
                                          Indels:          0
                                          Gaps:            0
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US-10-826-929A-1 (1-1061) x US-08-453-848-7 (1-570)

Qy    48 TTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCACCAGTGGAAACAACACAGCC 107
         |||:::  ::::::::  :::  |||  :::  |||:|||||||
Db    12 LeuValAlaValSerAsnAlaIleProGlyAspPheProGlyAsnAspAsnSerThrAla 31

Qy   108 ACATTATGTCTGGGACACCATGCAGTAGCAAATGGACAAATGGTAAAAACATAACTGAT 167
         |||||||||  :|| ||  ::::
Db    32 ThrLeuCysLeuGlyHisHisAlaValProAsnGlyThrLeuValLysThrIleThrAsn 51

Qy   168 GACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGCATTCAATGAGGGAAAATA 227
         |||||||||  |||  |||  ||||  ||:::|||
Db    52 AspGlnIleGluValThrAsnAlaThrGluLeuValGlnSerSerThrGlyArgIle 71

Qy   228 TGCAACAACTCATATAAAGTTCTAGATGGAAGAAAATTGCACATTAATAGATGCAATGCTA 287
         ||:::::: :::::::||||||||| |::||||||||
Db    72 CysAspSerProHisArgIleLeuAspGlyLysAsnCysThrLeuIleAspAlaLeuLeu 91

Qy   288 GGAGACCCCACTGTGATGTCTTCCAGTATGCAGAATTGGACCTTCTTCATAGAAAGAAGC 347
         ||||||||  :::  ||||||||||:||
Db    92 GlyAspProHisCysAspGlyPheGlnAsnLysGluTrpAspLeuPheValGluArgSer 111

Qy   348 AGCGCTTCAGCAATTGCTACCCATATGACAATCCTGACTATGCATCCATGCCTGCCTCCATT 407
         ||||||||||||  :::||||||||  ||| |||||:|
Db   112 LysAlaTyrSerAsnCysTyrProTyrAspValProAspTyrAlaSerLeuArgSerLeu 131

Qy   408 GTAGCATCCTCAGGAGACATTAGAATTCACAGCAGAGGGGATTCACATGGACAGGTGTCACT 467
         ||||||||||||| |||| :|| ||||:|
Db   132 ValAlaSerSerGlyThrLeuGluPheIleAsnGluAspPheAsnTrpThrGlyValAla 151

Qy   468 CAAAACGGAGAAGGTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTG 527
         ||||::|  |||||||| ::::|||||||||
Db   152 GlnAspGlyGlySerTyrAlaCysLysArgGlySerValAlaSerPheSerArgLeu 171

Qy   528 AATTGGCTAACAAAATCTGAAACTCTTACCCCACCACCATTGATGACAATGCCTACCAAT 587
         ||||||||  |||  |||||||||
Db   172 AsnTrpLeuHisLysSerGluTyrLysTyrProAlaLeuAsnValThrMetProAsnAsn 191

Qy   588 AAAAATTTCGACAAACTATACATCTCGGGGATTCATCACCCGAGCTCAAACCAACAGCAG 647
         |||||||||||||| ::::::::
Db   192 GlyLysPheAspLysLeuTyrIleTrpGlyValHisHisProSerThrAspArgAspGln 211

Qy   648 ACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAA 707
         ||||||||||||||| :::::::
Db   212 ThrSerLeuTyrValArgAlaSerGlyArgValThrValSerThrLysArgSerGlnSer 231

Qy   708 ACGATAGTCCCTAATATCGGATCTAGACCGTGGTTAGGGTCAATCAGCCAGGAGATAAGC 767
         ||:::::|||||| ||| ||||||||||
Db   232 ThrValThrProAsnIleGlySerArgProValArgGlySerSerArgIleSer 251

Qy   768 ATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATAAAACAGTAATGGCAACTTA 827
         ||||||||  :::||||||||
Db   252 IleTyrTrpThrIleValLysProGlyAspIleLeuLeuIleAsnSerThrGlyAsnLeu 271

Qy   828 GTTGCACCGCGGGATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGAT 887
         :::|||||||||| ||||||||||
Db   272 IleAlaProArgGlyThrTyrPheIleLysArgAsnGlyLysSerSerIleMetArgSerAsp 291

Qy   888 GCACCCATAGACAGCATTGTGTCTGTCAGAATGTATTACACCCAAATGGAGCATCCCAACGAC 947
         |||||||| :::||||||||||
Db   292 AlaProIleGlyThrCysSerSerGluCysIleThrProAsnGlySerIleProAsnAsp 311

Qy   948 AAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGCCCAAGTATATCAGGCAA 1007
         |||||||| :::||||||||||
Db   312 LysProPheGlnAsnValAsnArgIleThrTyrGlyAlaCysProArgTyrValLysGln 331

Qy  1008 AACACTTTAAAGCTGGCCACTGGCATGAGGAATATACCAGAAAAGCAAATCAGA 1061
         :::|||||||||| :::||||||||||
Db   332 AsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGluLysGlnThrArg 349
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RESULT 12
US-09-169-027-7

Query Match: 74.66%   Indels: 1
DB: 4   Gaps: 1

US-10-826-929A-1 (1-1061) x US-09-784-984B-53 (1-566)

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Qy      30 ATGAGAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAC---CCA 86
           ||||||||       :::      |||  ||||       ||       |||||||      :::
Db       1 MetLysThrValIleAlaLeuSerTyrIleProPheCysLeuValLeuGlyGlnAspLeuPro 20

Qy      87 ACCAGTGAAACAACACAGCCACATTATGTCTGGGACACCATGCAGTAGCAAATGGAACA 146
           :::||:::||||||       |||||       ||||       ||||||||||||
Db      21 GluAsnGlySerSerThrAlaLysProGlyLeuGlyHisHisAlaValProAsnGlyThr 40

Qy     147 TTGGTAAAACAATAACTGATGACCAAATGAGGTGACAAATGCTACTGAATTAGTTCAG 206
           ||||       |||||||       ||||       |||||       ||||       ||||
Db      41 LeuValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60

Qy     207 AGCATTCAATAGGAGAAAATATGCAACAACTCATATAAAGTTCTAGATGAAGAAATTGC 266
           |||      |||          :::::::::      ||
Db      61 SerPheSerMetGlyLysIleCysAsnAsnProHisArgValLeuAspGlyAlaAsnCys 80

Qy     267 ACATTAATAGATGCAATGCTAGGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGG 326
           |||      |||||||||:::||||||       ||       ||||       ||||||||
Db      81 ThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluLysTrp 100

Qy     327 GACCTCTTCATAGAAAAGAAGCAGCGGCTTTCAGCAATTGCTACCCATATGACATCCCTGAC 386
           ||||       ||||||||||       ||||||||       ||||||       ||||||
Db     101 AspLeuPheValGluLysArgSerLysPheSerAsnCysTyrProTyrAspValProAsp 120

Qy     387 TATGCATCGCTCCGGTCCATTGTGACATCCTCAGGAACATTAGAATTCAACAGCAGAGGGA 446
           ||||||||||       :::||||||       |||       ||||||||:::
Db     121 TyrAlaSerLeuArgSerLeuIleAlaSerSerGlyThrLeuGluPheIleAsnGluGly 140

Qy     447 TTCACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGATCAGCC 506
           ||||       :::||||       |||||||||       ||||||       ||||||
Db     141 PheAsnTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyProAsp 160

Qy     507 GATAGTTTCTTTAGCCGACTGAATTGGCTAACAACAAAATCTTACCCCACATTG 566
           |||          :::          ||||       |||||||:::||||||
Db     161 SerGlyPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnThrTyrProMetLeu 180
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RESULT 10
US-09-784-984B-53

; Sequence 53, Application US/09784984B
; Patent No. 657243
; GENERAL INFORMATION:
; APPLICANT: Merial Ltd.
; APPLICANT: Audonnet, Jean-Christophe
; APPLICANT: Bouchardon, Annabelle
; APPLICANT: Baudu, Philippe
; APPLICANT: Riviere, Michael
; TITLE OF INVENTION: Polynucleotide Vaccine Formula Against Porcine Reproductive and
; TITLE OF INVENTION: Respiratory Pathologies
; FILE REFERENCE: 454313-2230.1
; CURRENT APPLICATION NUMBER: US/09/784,984B
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: FR 96/09338
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01313
; PRIOR FILING DATE: 1997-07-15
; PRIOR APPLICATION NUMBER: US 6,207,165
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Swine Influenza Virus
US-09-784-984B-53

Alignment Scores:
Pred. No.:   7.55e-142   Length: 566
Score: 1427.50   Matches: 262
Percent Similarity: 85.51%   Conservative: 33
Best Local Similarity: 75.94%   Mismatches: 49

US-10-434-811A-8

Alignment Scores:
Pred. No.:   8.75e-180   Length: 565
Score: 1787.00   Matches: 333
Percent Similarity: 99.42%   Conservative: 9
Best Local Similarity: 96.80%   Mismatches: 2
Query Match: 93.46%   Indels: 0
DB: Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-434-811A-8 (1-565)

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Qy    30 ATGAGAGACAACCATTATTTGATACTACTGGGTCTCACAGTCAAACCCAACC 89
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Db     1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValThrSerGlnAsnProThr 20

Qy    90 AGTGGAACAACACAGCCACATTATGTCTGGGACACCATGCAGTAGCAAATGGAACATG 149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy   150 GTAAAACAATAACTGATGACGAACAAATGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy   210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAGTTCTAGATGGAAGAAATTGCACA 269
         |||||||||||||||||||||||||::::||||||||
Db    61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy   270 TTAATAGATGCAATGCCACTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
         ||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAGAAGAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
         |||||||||||||||::::||||||
Db   101 LeuPheIleGluGluGluGlnArgPheSerAlaPheSerTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTCACAGCAGAGGATTC 449
         ||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy   450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
         ||||||||||||||||||::::||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyArgSerGlySerAlaLysArgGly 160

Qy   510 AGTTTCTTTAGCGGACTGAATTGGCTAACAAAAATCTGGAACTTCTTACCCACCATTGAAT 569
         ||||||||||||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAATACTATACATCGGGGATTCATCACCCG 629
         ||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspAsnThrIleHisArgGlyIleIleThrHisProAspGln 200

Qy   630 AGCTCAAACCAACACAGAGAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689
         ||||||||::::||||||
Db   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220

Qy   690 ACAAAAGAGCTCAACAAACCATAGTCCCTAATATCCGGATCTAGACCGTGGTTAGGGGT 749
         ||||||||||||||||||||::::||||||
Db   221 ThrLysArgSerGlnThrIleLeuProAsnIleGlySerArgProArgValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACATTGTAAAACCTGAGATATCCTAATGATA 809
         |||||||||||||::::||||||
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGluIleAspAspMetIle 260

Qy   810 AACAGTAATGGCAACTAGTTGCACCGCGGGATATTTAAATTGAAAATCAGGGGAAAGC 869
         |||||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrTyrLysLeuLysSerGlyLysSer 280

Qy   870 TCTGTAATGAGATCAGAGTGTCACTCAAATGGTGTCACTCAAATGTAATACCACCAAAT 929
         ||||||||||||||||||||||||::::||||||
Db   281 SerValMetArgSerAspAlaProIleGlyTyrCysValSerGluCysIleThrProAsn 300

Qy   930 GGAAGCATCCCCAACGACAAAACCATTCAAAATGTGAACAAAGTGAACAAAATCGAAAATGC 989
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Db  261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuThrGlyLysSer 280

Qy  870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGTATTACCACCAAAT 929
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300

Qy  930 GGAGCATCCCAACGACAAACCATTCAAAATGTGACAAAGTTACATATGGAAAATGC 989
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy  990 CCCAAGTATATCAGGCAGGATAAGCTGGATGGAGAATATACCAGAA 1049
        ||||||||||||||||||||||||||||||||||||||| :::||
Db  321 ProLysTyrIleArgGlnAspLysLeuAspGlyGluTyrThrMetArgAsnValProGlu 340

Qy 1050 AAGCAAATCAGA 1061
        ||||||||||||
Db  341 LysGlnIleArg 344
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RESULT 7
US-10-065-133A-8.
; Sequence 8, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-8

Alignment Scores:
Pred. No.:	8.75e-180	Length:	565
Score:	1787.00	Matches:	333
Percent Similarity:	99.42%	Conservative:	9
Best Local Similarity:	96.80%	Mismatches:	2
Query Match:	93.46%	Indels:	0
DB:		Gaps:	0

US-10-826-929A-1 (1-1061) x US-10-065-133A-8 (1-565)

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Qy   30 ATGAGAGACAACACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCGAAAACCACC 89
        ||||||||||||||||||||        |||||||||||||||||||||
Db    1 MetLysThrThrIleIleLeuIleLeuProLeuThrHisTrpSerGlnAsnProThr 20

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGACACCAGCAGTAGCAAATGAACATTG 149
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy  150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy  210 ATTTCAATAGGAGAAAATGCACAACACTCATATAAAGTTCTAGAATGAAGAAATTGCACA 269
        ||||||||||||||||||||||||||| :::|||||||||||||||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuGlyArgAsnCysThr 80

Qy  270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGGTCTTCCAGTATGAGAATTGGGAC 329
        ||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyTyrAspProHisCysAspGluPheGlnTyrGluAsnTrpAsp 100

Qy  330 CTCTTCATAGAAAGAAGCAGCGCCTTCAGCAATTGCTACCCATATGAACATCCCTGACTAT 389
        ||||||||||||||||||||||||||||||||||| :::||
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Db  101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyrProTyrAspIleProAspTyr 120

Qy  390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGACATCCCAGGAATTCACAGCAGAGGGATTC 449
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy  450 ACATGGACAGGTGTCACTCAAAACCGAAGAGAGTGGACCTGCAAAAGGGGATCAGCCGAT 509
        |||||||||||||||||||||||||||||||| :::||||||||||||||
Db  141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp 160

Qy  510 AGTTTCTTAGCCGACTGAATTGGCTAACAAAATCTGGAGAAATCTTTACCCACATTGAAT 569
        |||||||||||||||||||||||||||||||||||||||
Db  161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180

Qy  570 GTGACAATGCCTACAATAAAAATTTGACAAACTATACATCTGGGGATTCATCACCCCG 629
        |||||||||||||||||||||||||||||||||||||||
Db  181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy  630 AGTCAAACCAACACGACAGAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689
        |||||||||||||||| :::||||||||||||||||||
Db  201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220

Qy  690 ACAAAAGAAGTCAACAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTAGGGGT 749
        ||||||||||||||||||||||||||||||||||||||||||||
Db  221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProValArgGly 240

Qy  750 CAATCAGGCAGGATAAGCATATACTGGGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
        |||||||||||||||||||||||||||||||||||||||||
Db  241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

Qy  810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTTAAATTGAAACAGGGAAAAGC 869
        |||||||||||||||||||||||||||||||||||||||||
Db  261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280

Qy  870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGTATTACCACCAAAT 929
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300

Qy  930 GGAGCATCCCAACGACAAACCATTCAAAATGTGACAAAGTTACATATGGAAAATGC 989
        |||||||||||||||||||||||||||||||||||||||||||||
Db  301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy  990 CCCAAGTATATCAGGCAGGATAAGCTGGATGGAGAATATACCAGAA 1049
        |||||||||||||||||||||||||||||| :::||
Db  321 ProLysTyrIleArgGlnAspLysLeuAspGlyGluTyrThrMetArgAsnValProGlu 340

Qy 1050 AAGCAAATCAGA 1061
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Db  341 LysGlnIleArg 344
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RESULT 8
US-10-434-811A-8
; Sequence 8, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8

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Qy   270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAGAGAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
             ||||||||||    |||||    |||:::||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerCysTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
             ||||||||||||    |||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy   450 ACATGACACAGTGTCACTCAAAACGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
             ||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyArgSerCysLysArgGlySerAlaAsp 160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCACATTGAAT 569
             ||||||||||||||||:::||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACACTCGGGGATATCCTAATGATA 629
             ||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleArgGlyIleProAsnHisPro 200

Qy   630 AGCTCAAACCAACACCAGCCAGAATTGTACATCCAAGATGCAGTAACAGTCTCA 689
             ||||||||||    |||:::||||||||||||||||||||||||||||
Db   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnAspGlyValThrValSer 220

Qy   690 ACAAAAGAAGTCAACAACAGCATAGTCCCTAATATCGGATCTGAGTGCTCTCA 749
             ||||||||||||||:::||||||||||||||||||||||||||
Db   221 ThrLysGluGluArgSerGlnGlnThrIleIleProAsnIleGlySerGluCysSer 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATA 809
             ||||||||||||:||||||||||||||||||||||||||
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

Qy   810 AACAGTAATGCAACTTAGTTGCACCGCGGGATATTTTAAATTGAAAACAGGAAAAGC 869
             ||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuValAlaProAlaGlyTyrPheLysLeuLysThrGlyLysSer 280

Qy   870 TCTGTAATGATGACATGCACCCATAGATGCTTTGTGTGCTGAATGTATTACACCCAAAT 929
             ||||||||||||||||||:::||||||||||||||
Db   281 SerValMetArgSerAspAlaProIleAspAlaCysValSerGluCysIleThrProAsn 300

Qy   930 GGAAGCATCCCCAACGACAAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
             |||||||||||||||||||||||||||||||||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy   990 CCCAAGTATATCAGGCAAAACACTTTAAAGTGGGATGAGGAGAATTACCAGAA 1049
             ||||||||||||||||:::||||||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340

Qy  1050 AAGCAAATCAGA 1061
             ||||:||||
Db   341 LysGlnIleArg 344
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RESULT 6
US-09-762-861B-8

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;   Sequence 8, Application US/09762861B
;   Patent No. 6579528
;   GENERAL INFORMATION:
;   APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
;   APPLICANT: Education
;   APPLICANT: Dowling, Patricia W.
;   APPLICANT: Youngner, Julius S.
;   TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;   FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
;   CURRENT APPLICATION NUMBER: US/09/762, 861B
;   CURRENT FILING DATE: 2001-02-13
;   PRIOR APPLICATION NUMBER: PCT/US99/18583
;   PRIOR FILING DATE: 1999-08-12
;   PRIOR APPLICATION NUMBER: 09/133,921
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;   PRIOR FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 8
;     LENGTH: 565
;     TYPE: PRT
;     ORGANISM: Equine influenza virus H3N8
US-09-762-861B-8

Alignment Scores:
Pred. No.:                                    Length:       565
Score:                     8.75e-180          Matches:      333
Percent Similarity:        1787.00            Conservative:   9
Best Local Similarity:     99.42%             Mismatches:     2
Query Match:               96.80%             Indels:         0
DB:                        93.46%             Gaps:           0
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US-10-826-929A-1 (1-1061) x US-09-762-861B-8 (1-565)

```
Qy    30 ATGAAGACAACCATTATTTTGATACTACTGGCACCCATTGGGCTCACAGTCAAAACCCAACC 89
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetLysThrThrIleIleLeuIleLeuLeuAlaProHisTrpLeuThrValLysGlnAsnProThr 20

Qy    90 AGTGGAAACAACACAGCCACATTATGCTGGGACACCATGCAGTAGCAGAACATTG 149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy   210 ATTTCAATAGGGAAAATATGCAACACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
             |||||||||||||||||||||||||||||||:::||||||||||||||||
Db    61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy   270 TTAATGATGCAATGCTAGGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAGAGAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
             ||||||||||    |||:::||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerCysTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy   450 ACATGACACAGTGTCACTCAAAACGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
             ||||||||||||||||||||:::||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyArgSerCysLysArgGlySerAlaAsp 160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCACATTGAAT 569
             ||||||||||||||||:::||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTCGGGGATTCATCACCCG 629
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleArgGlyIleHisHisPro 200

Qy   630 AGCTCAAACCAACACCAGCCAGAATTGTACATCCAAGATGGAGTAACAGTGTCATCA 689
             ||||||||    ||::::||||||||||||||||||||||||||
Db   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnAspGlySerAsnGlyValThrValSer 220

Qy   690 ACAAAAGAAGTCAACAACAGCATAGTCCCTAATATCGGATCTGAGTGCTCTCA 749
             ||||||||||||||:::||||||||||||||||||||||||||
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerGluArgGlyValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATA 809
             ||||||||||||||||||||||||||||||||||||||||||||
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

Qy   810 AACAGTAATGCAACTTAGTTGCACCGCGGGATATTTTAAATTGAAAACAGGAAAAGC 869
             |||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuValAlaProAlaGlyTyrPheLysLeuLysThrGlyLysSer 280

Qy   870 TCTGTAATGATGACATGCACCCATAGATGCTTTGTGTGCTGAATGTATTACACCCAAAT 929
             ||||||||||||||||||:::||||||||||||||
Db   281 SerValMetArgSerAspAlaProIleAspAlaCysValSerGluCysIleThrProAsn 300

Qy   930 GGAAGCATCCCCAACGACAAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
             |||||||||||||||||||||||||||||||||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy   990 ACATGACAGTGTCACTCAAAACGAAGAGAGTGGAGCCGCCCAAAAGGGATCAGCCGCGAT 509
             ||||||||||||||||||||||||||||||||||||||:::||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyArgSerCysLysArgGlySerAlaAsp 160

Qy   510 AGTTCTTAGCCGACTGAATTGGCTGAATGGCTAACAAAATCTGGAAACTCTTACCCACATTGAAT 569
             ||||||||||||||||:::||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTCGGGGATTCATCACCCG 629
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleArgGlyIleHisHisPro 200

Qy   630 AGCTCAAACCAACACCAGCCAGAATTGTACATCCAAGATGGAGTAACAGTGTCATCA 689
             |||||||||::::::||||||||||||||||||||||||||||
Db   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnAspGlySerAsnGlyValThrValSer 220

Qy   690 ACAAAAGAAGTCAACAACAGCATAGTCCCTAATATCGGATCTGAGCGAGGGATTC 449
             ||||||||||||:::||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerCysTyrProTyrAspIleProAspTyr 120

Qy   690 ACAAAAGAAGTCAACAACAGCATAGTCCCTAATATCGGATCTGAGTGCTCTCA 749
             :|||||||||||||::::||||||||||||||||||||||||||
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerGluArgGlyValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATA 809
             |||||||||||||||||||||||||||||||||||||||||||||
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260
```

Alignment Scores:
Pred. No.:   1.6e-180   Length: 565
Score: 1794.00   Matches: 333
Percent Similarity: 99.42%   Conservative: 9
Best Local Similarity: 96.80%   Mismatches: 2
Query Match: 93.83%   Indels: 0
DB: Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-434-811A-11 (1-565)

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCAACC   89
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetLysThrThrIleIleLeuIleLeuIleLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy   90 AGTGGAAACAACAGCCACATTATGTCTGGGACACCATGTCAGTAGCAGTGCAAATGGAACATTG   149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaValAlaAsnGlyThrLeu   40

Qy 150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC   209
         ||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy 210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA   269
         ||||||||||||||||||||||||||||||||||||||||||||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr   80

Qy 270 TTAATAGATGCAATGCTAGGAGACACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC   329
         ||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyAspHisCysAspValPheGlnTyrGluAsnTrpAsp   100

Qy 330 CTCTTCATAGAAAGAGAGCAGCGCTTTCAGCAATTGCTACCATATGACATCCCTGACTAT   389
         |||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db 101 LeuPheIleGluArgSerAlaPheSerSerGlnCysTyrProTyrAspIleProAspTyr   120

Qy 390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGAACATTAGAATTCACAGCAGAGGGATTC   449
         ||||||||||||||||||||||||||||||||||||
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe   140

Qy 450 ACATGGACAGGTGTCACTCAAAACGGAGGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT   509
         |||||||||||||||||||||||||||||:::|||||:||
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGluSerAlaAsp   160

Qy 510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTGAAT   569
         |||||||||||||||||||:::|||||||||||||||
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerTyrProThrLeuAsn   180

Qy 570 GTGACAATGCCTAACAATAAAAATTCGACAAACTATCATCTGGGGATTCATCACCCG   629
         |||||||||||||||||||||||||||||||||||||||||||||
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysTyrLeuTyrIleTrpGlyIleHisHisPro   200

Qy 630 AGCTCAAACCAACAGCAGACAGAGATTGTCATCCAAGAATCAGAGGAGTAACAAGTCTCA   689
         ||||||||:::||||||||||||||||||
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer   220

Qy 690 ACAAAAAGAGAGTCAACAACGATAGTCCCTAATATCGGATCTGGGGTAGGGGT   749
         ||||||||||||||||||||||||||||||||||||:::|
Db 221 ThrLysArgSerGlnIleThrIleIleGluProAsnIleGlySerArgProValArgGly   240

Alignment Scores:
Pred. No.:   8.75e-180   Length: 565
Score: 1787.00   Matches: 333
Percent Similarity: 99.42%   Conservative: 9
Best Local Similarity: 96.80%   Mismatches: 2
Query Match: 93.46%   Indels: 0
DB: Gaps: 0

US-10-826-929A-1 (1-1061) x US-09-506-286B-8 (1-565)

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCAACC   89
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetLysThrThrIleIleLeuIleLeuIleLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy   90 AGTGGAAACAACAGCCACATTATGTCTGGGACACCATGTCAGTAGCAGTGCAAATGGAACATTG   149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaValAlaAsnGlyThrLeu   40

Qy 150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC   209
         ||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy 210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA   269
         ||||||||||||||||||||||||||||||||||::::||||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr   80

Qy 750 CAATCAGGACAGGATAAGACATATCTGGACCCATTGTAAAAACCTGGAGATATCCTAATGATGA   809
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuThrIle   260

Qy 810 AACAGTAATGGCAACTAGTTGCACCGCGGGATATTTAAATTGAAACAGGGAAAAGC   869
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgArgGlyTyrPheLysLysThrGlyLysSer   280

Qy 870 TCTGTAATGAGATCAGATCAGACCACCATAGACATTTGTGTCTCGAATGTATTACCACAAAT   929
         |||||||||||||||||||||||||||||||||
Db 281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn   300

Qy 930 GGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC   989
         |||||||||||||||||||||||||||||||||||||||||||||||||:::|
Db 301 GlySerIleProAsnAspLysProPheGlnAsnThrGlyLeuAlaThrGlyLysLysCys   320

Qy 990 CCCAAGTATATCAGGCAAAACACTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA   1049
         ||||||||||||||||||||||||||||||||||:::||||||||||||||
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu   340

Qy 1050 AAGCAAATCAGA   1061
         ||||||||||||
Db 341 LysGlnIleArg   344

Db |||||||||||||||||||||||
Qy   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnSerGlyArgValThrValSer 220

Db   689 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAGCAGAGTAACAGTCTCA 689
Qy   210 ATTTCAATAGGAGAAAATGCAACAACTCATATAAAGTTCTAGATGGAGAAAATTGCACA 269

Qy   630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAGCAGAGTAACAGTCTCA 689
Db   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnSerGlyArgValThrValSer 220

Qy   690 ACAAAAAGAGAGTCAACAAACAGATAGTCCCTAATATCGGATCCAGAACCGTGGGTTAGGGGT 749
Db   221 ThrLysArgGlnThrLysSerAsnIleGlyHisProValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCAATTGTAAAACCTGGAGATATCCTAATGATA 809
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrThrLeuValLysProGlyAspIleLeuThrIle 260

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC 869
Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuThrGlyLysSer 280

Qy   870 TCTGTAATGAGATCAGATGACCCCATAGACATTTGTGTGTCGAAATGTTATTACCAAAAT 929
Db   281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300

Qy   930 GGAAGCATCCCCAACGACAAACACTTTAAAGTGGCCACTGGAGGAATATACCAGAA 989
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAlaThrGlyGlyIleTyrGlnLysCys 320

Qy   990 CCCAAGTATATCAGGCAAATCAGGCAAATCAGGATAGGAATATACCAGAA 1049
Db   321 ProLysTyrIleArgGlnAsnThrLysLeuTyrMetArgAsnValProGlu 340

Qy   1050 AAGCAAATCAGA 1061
Db   341 LysGlnIleArg 344

Alignment Scores:
Pred. No.:   1.6e-180   Length: 565
Score: 1794.00   Matches: 333
Percent Similarity: 99.42%   Conservative: 9
Best Local Similarity: 96.80%   Mismatches: 9
Query Match: 93.83%   Indels: 0
DB: 4   Gaps: 0

US-10-826-929A-1 (1-1061) x US-10-065-133A-11 (1-565)

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCAACC 89
Db   1 MetLysThrThrIleIleLeuIleLeuLeuThrHisThrTyrSerGlnAsnProThr 20

Qy   90 AGTGTGAAAACAACACAGCCACATATGTCTCTGGGACAACCATCCAGTAGCAAATGGAACATTG 149
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAlaGlyThrLeu 40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209

Db ||||||||||||||||||||||||
Qy   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy   210 ATTCAATAGGAGAAAATGCAACAACTCATATAAAGTTCTAGATGGAGAAAATTGCACA 269
Db   61 IleSerIleGlyLysLysCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy   270 TTAATAGATGCAATGCTAGGAGCACCCCACTGTGATCGTCTTCCAGTATGAGAATTGGGAC 329
Db   81 LeuIleAspAlaMetLeuGlyAlaProProHisCysAspArgValPheGlnTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAGAAGCAGCAGGGCGTTTCAGCAATTGCTACCCATATGACATCCTGACTAT 389
Db   101 LeuPheIleGluArgSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy   450 ACATGACAGGTGTCACTCAAAACGAAGAGTGGAGCCTGCAAAACGGGATCAGCCGAT 509
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGluSerAlaAsp 160

Qy   510 AGTTCTTAGCCGACTGAAATTGGCTAACAAAATCTTACCCCACATTGAAT 569
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAACTATACATCTGGGGATTCATCACCCG 629
Db   181 ValThrMetProAsnAsnLysAsnPheAspAsnTyrIleSerTrpGlyIleHisHisPro 200

Qy   630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAGCAGAGTAACAGTCTCA 689
Db   201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnSerGlyArgValThrValSer 220

Qy   690 ACAAAAAGAGAGTCAACAAACAGATAGTCCCTAATATCGGATCCAGAACCGTGGGTTAGGGGT 749
Db   221 ThrLysArgGlnThrLysSerAsnIleGlyHisProValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCAATTGTAAAACCTGGAGATATCCTAATGATA 809
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrThrLeuValLysProGlyAspIleLeuThrIle 260

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC 869
Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuThrGlyLysSer 280

Qy   870 TCTGTAATGAGATCAGATGACCCCATAGACATTTGTGTGTCGAAATGTTATTACCAAAAT 929
Db   281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300

Qy   930 GGAAGCATCCCCAACGACAAACACTTTAAAGTGGCCACTGGAGGAATATACCAGAAATGC 989
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAlaThrGlyGlyIleTyrGlnLysCys 320

Qy   990 CCCAAGTATATCAGGCAAAACACTTTAAAGTGGCCACTGGAGGAATATACCAGAA 1049
Db   321 ProLysTyrIleArgGlnAsnThrLysLeuTyrMetArgAsnValProGlu 340

Qy   1050 AAGCAAATCAGA 1061
Db   341 LysGlnIleArg 344

Alignment Scores:
Pred. No.:   1.6e-180   Length: 565
Score: 1794.00   Matches: 333
Percent Similarity: 99.42%   Conservative: 9
Best Local Similarity: 96.80%   Mismatches: 2
Query Match: 93.83%   Indels: 0
DB: 4   Gaps: 0

US-10-826-929A-1 (1-1061) x US-09-762-861B-11 (1-565)

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Qy   30  ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAAACC   89
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy   90  AGTGGAAACAACACAGCCACCATTATGTCTGGGACACCATTGGTACACCATTG        149
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21  SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy  150  GTAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC    209
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41  ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy  210  ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAAATTGCACA    269
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyGluAsnCysThr   80

Qy  270  TTAATAGATGCAATGCTAGGAGACACCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC    329
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81  LeuIleAspAlaMetLeuGlyAspProHisCysAspGlyPheGlnTyrGluAsnTrpAsp   100

Qy  330  CTCTTCATAGAAAGAAGCAGCGCGTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT    389
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101  LeuPheIleGluArgSerSerAlaPheSerAlaThrLeuProProTyrProTyrAspTyr   120

Qy  390  GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGACAATAGAATTCACAGCAGAGGGATTC    449
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheHisAlaGluGlyPhe   140

Qy  450  ACAATGGACAGGTGTCACTCAACAAACGGAAGAGTGACTGAGAAGTGGAGCCTGCAAAAGG    509
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141  ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGluSerAlaAsp   160

Qy  510  AGTTCTTTAGCCGACTGAATTGCTAACAAAATCTTACCCCACATTGAAT               569
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  161  SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn   180
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Db    1  MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy   90  AGTGGAAACAACACAGCCACCATTATGTCTGGGACACCATTGGTACACCATTG        149
Db   21  SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy  150  GTAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC    209
Db   41  ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy  210  ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAAATTGCACA    269
Db   61  IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyGluAsnCysThr   80

Qy  270  TTAATAGATGCTAGGAGACGCCGTTCCAGCAATTGCTACCCATATGACATCCCTGACTAT    329
Db   81  LeuIleAspAlaMetLeuGlyAspProHisCysAspGlyPheGlnTyrGluAsnTrpAsp   100

Qy  330  GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGACAATAGAATTCACAGCAGAGGGATTC    389
Db  101  LeuPheIleGluArgSerSerAlaPheSerAlaThrLeuProProTyrProTyrAspTyr   120

Qy  390  GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGACAATAGAATTCACAGCAGAGGGATTC    449
Db  121  AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheHisAlaGluGlyPhe   140

Qy  450  ACAATGGACAGGTGTCACTCAACAAACGGAAGAGTGACTGAGAAGTGGAGCCTGCAAAAGG    509
Db  141  ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGluSerAlaAsp   160

Qy  510  AGTTCTTTAGCCGACTGAATTGCTAACAAAATCTTACCCCACATTGAAT               569
Db  161  SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn   180

Qy  570  GTGACAATGCCTAACAATAAAATTCGACAAACTATCATCTGGGGATTCATCACCCG        629
Db  181  ValThrMetProAsnAsnLysIleArgGlnThrIleIleTrpGlyIleHisHisPro   200

Qy  630  AGTCCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAGAGTGACTGAGAGTCTCA    689
Db  201  SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer   220

Qy  690  ACAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT    749
Db  221  ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly   240

Qy  750  CAATCAGGCAGGAGTAAGCACATATACTGGACCATTGTAAAACCTGGAGATCCTAATGATA    809
Db  241  GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspProAsnIleThr   260

Qy  810  AACAGTAATGGCAACTAGTTGCACCGCGGGGGATATTTAAATTGAAAACAGGAGAAAGC    869
Db  261  AsnSerAsnGlyAsnLeuValAlaProAsnGlyTyrPheLysIleLysThrGlyLysSer   280

Qy  870  TCTGTAATGAGATCAGATGCACCCATAGACAATTGTGTCTGAATGTATTACACCAAAT    929
Db  281  SerValMetArgSerAspAlaProIleAspAsnCysValSerGluCysIleThrProAsn   300

Qy  930  GGAAGGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC    989
Db  301  GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys   320

Qy  990  CCCAAGTATATCAGGCAGAAACACTTAAAGCTGGCCACTGGATGAGGAATATACCAGAA    1049
Db  321  ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu   340

Qy  1050 AAGCAAAATCAGA    1061
Db  341  LysGlnIleArg    344
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                    GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on:      February 27, 2005, 18:16:22 ; Search time 40 Seconds
                                         (without alignments)
                              3960.133 Million cell updates/sec

Title:         US-10-826-929A-1
Perfect score: 1912
Sequence:      1 agcaaagcaggggatatt.........taccagaaaagcaaatcaga 1061

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext   0.5
                Ygapop 10.0 , Ygapext   0.5
                Fgapop  6.0 , Fgapext   7.0
                Delop   6.0 , Delext    7.0

Searched:      513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:      1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
               ; Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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 -Qe/cgn2_1/USPTO_spool_p/US10826929/runat_27022005_095244_27608/app_query.fasta_1.1223
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 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPEXT=0.5 -YGAPOP=10 -DELOP=6 -DELEXT=7

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        3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                             SUMMARIES
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1	1794	93.8	565	4	US-09-506-286B-11	Sequence 11, Appl
2	1794	93.8	565	4	US-09-762-861B-11	Sequence 11, Appl
3	1794	93.8	565	4	US-10-065-133A-11	Sequence 11, Appl
4	1794	93.8	565	4	US-10-434-811A-11	Sequence 11, Appl
5	1787	93.5	565	4	US-09-506-286B-8	Sequence 8, Appli
6	1787	93.5	565	4	US-09-762-861B-8	Sequence 8, Appli
7	1787	93.5	565	4	US-10-065-133A-8	Sequence 8, Appli
8	1787	93.5	565	4	US-10-434-811A-8	Sequence 8, Appli
9	1427.5	74.7	566	3	US-09-232-468A-22	Sequence 22, Appl
10	1427.5	74.7	566	4	US-09-784-984B-53	Sequence 53, Appli
11	1421	74.3	570	3	US-08-453-848-7	Sequence 7, Appli
12	1421	74.3	570	3	US-09-169-027-7	Sequence 7, Appli
13	1404.5	73.5	571	2	US-08-453-848-15	Sequence 15, Appl
14	1404.5	73.5	571	3	US-09-169-027-15	Sequence 15, Appl
15	1398.5	73.1	571	2	US-08-453-848-21	Sequence 21, Appl
16	1398.5	73.1	571	3	US-09-169-027-21	Sequence 21, Appl
17	1373	71.8	347	3	US-09-217-293-1	Sequence 1, Appli
18	624.5	32.7	569	3	US-08-686-968C-227	Sequence 227, App
19	588	30.8	566	3	US-09-232-468A-14	Sequence 14, Appl
20	588	30.8	566	4	US-09-784-984B-51	Sequence 51, Appl
21	580	30.3	572	2	US-08-453-848-9	Sequence 9, Appli
22	580	30.3	572	3	US-09-169-027-9	Sequence 9, Appli
23	393	20.6	347	1	US-08-229-781-58	Sequence 58, Appl
24	393	20.6	347	1	US-08-630-918-58	Sequence 58, Appl
25	393	20.6	347	4	US-09-004-422-58	Sequence 58, Appl
26	393	20.6	347	4	US-09-918-568-58	Sequence 58, Appl
27	321.5	16.8	165	1	US-08-120-607A-7	Sequence 7, Appli
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34	207.5	10.9	345	1	US-07-954-840A-18	Sequence 18, Appl
35	206.5	10.8	345	2	US-07-954-840A-12	Sequence 12, Appl
36	204	10.7	586	2	US-08-453-848-19	Sequence 19, Appl
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39	200.5	10.5	345	1	US-07-954-840A-14	Sequence 14, Appl
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41	199.5	10.4	345	1	US-07-954-840A-8	Sequence 8, Appli
42	198.5	10.4	345	1	US-07-954-840A-16	Sequence 16, Appl
43	198.5	10.4	345	1	US-07-954-840A-31	Sequence 31, Appl
44	195.5	10.2	345	1	US-07-954-840A-26	Sequence 26, Appl
45	194.5	10.2	345	1	US-07-954-840A-20	Sequence 20, Appl

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                                ALIGNMENTS

RESULT 1
US-09-506-286B-11
; Sequence 11, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
;  APPLICANT:  Dowling, Patricia W.
;  APPLICANT:  Youngner, Julius S.
;  APPLICANT:  The University of Pittsburgh, of the Commonwealth
;  TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
;  FILE REFERENCE: EQ-1-C2
;  CURRENT APPLICATION NUMBER: US/09/506,286B
;  CURRENT FILING DATE:  2000-02-16
;  PRIOR APPLICATION NUMBER: 09/133,921
;  PRIOR FILING DATE: 1998-08-13
;  PRIOR APPLICATION NUMBER: PCT/US99/18583
;  PRIOR FILING DATE: 1999-08-12
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;  LENGTH: 565
;  TYPE: PRT
;  ORGANISM: Equine influenza virus H3N8
US-09-506-286B-11

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US-10-826-929A-1 (1-1061) x US-09-506-286B-11 (1-565)

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```

```
XX
DT   28-OCT-1998   (first entry)
XX
DE   SIV strain H3N2 haemagglutinin.
XX
KW   Multivalent vaccine; pig; pathogen; respiratory disease; SIV; PRRSV;
KW   HCV; digestive disease; Aujeszky's disease virus; pseudorabies virus;
KW   vaccine; suid herpesvirus 1; swine influenza virus; hog cholera virus;
KW   vector; porcine respiratory and reproductive syndrome virus;
KW   haemagglutinin; SIRSV; swine infertility and respiratory syndrome virus;
KW   Actinobacillus pleuropneumoniae.
XX
OS   Swine influenza virus.
XX
PN   FR2751224-A1.
XX
PD   23-JAN-1998.
XX
PF   19-JUL-1996;   96FR-0009338.
XX
PR   19-JUL-1996;   96FR-0009338.
XX
PA   (INMR ) RHONE MERIEUX SA.
XX
DR   WPI; 1998-112824/11.
DR   N-PSDB; AAV49298.
XX
PT   Multi-valent polynucleotide vaccines for pigs - consist of at least 3
PT   plasmids able to express protective antigens from specified viruses.
XX
PS   Example 12; Fig 10; Fig 12; 63pp; French.
XX
CC   The invention relates to a multivalent vaccine for protecting pigs
CC   against several pathogens, especially pathogens associated with
CC   respiratory and digestive diseases. The pathogens are especially selected
CC   from Aujeszky's disease virus, swine influenza virus (SIV), porcine
CC   respiratory and reproductive syndrome virus (PRRSV), hog cholera virus
CC   (HCV) and Actinobacillus pleuropneumoniae. The vaccines are preferably
CC   composed of polynucleotide sequences encoding 3 antigens, all as part of
CC   vectors. This sequence represents the SIV strain H3N2 haemagglutinin
CC   protein. The coding sequence was subcloned into the plasmid pVR1012 to
CC   generate plasmid pPB144 for use in the vaccine
XX
SQ   Sequence 566 AA;
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Alignment Scores:

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Search completed: February 27, 2005, 18:24:54
Job time : 198 secs

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XX
AC   AAW68406;

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Qy 1044 CCAGAAAAGCAAATCAGA 1061
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Db   324 ProGluLysGlnThrArg 329

RESULT 14
ABP53896
ID   ABP53896 standard; protein; 329 AA.
XX
AC   ABP53896;
XX
DT   07-JAN-2003 (first entry)
XX
DE   Influenza A virus (A/Bangkok/25/(H3N2)) haemagglutinin partial protein.
XX
KW   Influenza; influenza A virus; pathogenicity; RNA viral disease;
KW   viral infection; selenium; vaccine; virucide; anti-HIV.
XX
OS   Influenza A virus.
XX
PN   WO200278717-A2.
XX
PD   10-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-EP003025.
XX
PR   28-MAR-2001; 2001US-00819387.
XX
PA   (NEST) SOC PROD NESTLE SA.
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Beck M, German B, Levander O, Van Dael P;
XX
DR   WPI; 2002-759948/82.
DR   N-PSDB; ABQ82725.
XX
PT   Treatment of influenza or reducing the risk of contracting influenza
PT   involves administering selenium to an individual.
XX
PS   Example 1; Page; 31pp; English.
XX
CC   The present invention describes a method for treating influenza or
CC   reducing the risk of contracting influenza, which involves administering
CC   selenium to an individual. Also described is a method for enhancing the
CC   efficacy of a viral vaccine by administering an antioxidant, preferably
CC   selenium, to an individual receiving the viral vaccine. The method can be
CC   used for treating influenza, for reducing the risk of contracting
CC   influenza, and for enhancing the efficacy of viral vaccine (preferably
CC   influenza vaccine) in an infant, elderly, a patient or a pet. It can also
CC   be used for treating virus such as coxsackie and HIV virus. The method
CC   provides an improved treatment for viral infection, by reducing in vivo
CC   mutations of the RNA virus. The method also improves a vaccine used to
CC   prevent transmission of an RNA viral disease. The present sequence
CC   represents the haemagglutinin protein from Influenza A virus
CC   (A/Bangkok/25/(H3N2)). N.B. The present sequence is not given in the
CC   specification, but is taken from the Genbank accession number AF008901,
CC   as specified on page 7
XX
SQ   Sequence 329 AA;

Alignment Scores:
Pred. No.:   5.24e-135   Length: 329
Score: 1436.00   Matches: 256
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US-10-826-929A-1 (1-1061) x ABP53896 (1-329)

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SQ   Sequence 329 AA;

Alignment Scores:
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Qy   264 TGCACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAAT 323
          ||||||:::|||||||||||||||:::|||||||||||||||||||||||||||||||
Db    64 CysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluLys 83

Qy   324 TGGGACCTCTTCATAGAAAGAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCT 383
          ||||||||:::|||||||||||||||||||||||||||||  |||||||
Db    84 TrpAspLeuPheValGluArgSerLysAlaPheSerAsnCysThrTyrProTyrAspValPro 103

Qy   384 GACTATGCATCGTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAG 443
          |||||||||||||:::|||||||||||||||||||||||||||||||||:||:|||
Db   104 AspTyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleAsnGlu 123

Qy   444 GGATTCACATGACAGTGTCACTCAAAAACGAAGAGTGGAGCCTGCAAAAGGGGATCA 503
          ||||| |||||||||||||||||||||||||||||:::|||||||:|||||:||||
Db   124 GlyPheAsnTrpThrGlyValThrGlnSerGlyGlySerTyrAlaCysLysArgGlySer 143

Qy   504 GCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACA 563
          ||:::|||||||||||||||||:::|||||||||||||    ||||||||
Db   144 ValAsnSerPhePheSerArgLeuAsnTrpLeuTyrLysSerGluTyrLysTyrProAla 163

Qy   564 TTGAATGTGACAATGCCTAACATAAAAAATTTCGACAACAATAACATCTGGGGATTCAT 623
          ||||||||||||||||::::||||||||||||||||||||||||||||:::|||||||
Db   164 LeuAsnValThrMetProAsnAsnGlyLysPheAspLysLeuTyrIleTrpGlyValHis 183

Qy   624 CACCCGAGCTCAAACCAACACCAGCAGAATTGTACATCCAAGAATCAGGACGAGTAACA 683
          ||||||:::|||||||||||::::|||||||||||||||:::||:::
Db   184 HisProSerThrGluLysGluGlnThrAsnLeuTyrValArgAlaSerGlyValThr 203

Qy   684 GTCTCAACAAAAGAGTCAACAAACAGATAGTCCCTAATATCGGATCTAGACCGTGGGTT 743
          |||||||||||||||||||||||||||  ||||||||||||||||||| |||||||
Db   204 ValSerThrLysArgSerGlnGlnThrValIleProAsnIleGlySerArgProTrpVal 223

Qy   744 AGGGGTCAATCAGGCAGGATAAGACCATTGTAAAACCTGGAGATATCCTA 803
          ||||| ||||||||||||  ||||||||:::||||||||||||||||:::
Db   224 ArgGlyLeuSerSerArgIleSerIleSerIleTyrTrpThrIleValLysProGlyAspIleLeu 243

Qy   804 ATGATAAACAGTAATGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGG 863
          ::|||||||||||||||||||:::||||||||||||||||||||||||:::|||
Db   244 LeuIleAsnSerThrGlyAsnAlaThrLeuValAlaProArgGlyTyrPheLysIleArgThrGly 263

Qy   864 AAAAGCCTGTAATGAGATCGATGAATGCACCCATAGACATTTGTGTCGTGAATGTATTACA 923
          ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db   264 LysSerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThr 283

Qy   924 CCAAATGGAAGCATCCCAACGACAAACCATTTCAAAATGAACAAAGTTACATATGGA 983
          |||||||||||||||||||:::|||||||||||||||||||||:::|||||||
Db   284 ProAsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGly 303

Qy   984 ACATATGATGATAAACAGTAATGGCAACTCGTAATGAGATCAGATCAGACATTTGTGTCGTCTGAA 854
          ||||||| ||||:::||||||||||||||||:::|||||||||||||||||:::||||
Db   241 AspIleLeuLeuAsnGlyAsnLeuIleAlaProArgGlyAsnGlyAsnLeuIleAlaProArgGlyAsnGlyTyrPheLysIle 260

Qy   855 AAAACAGGGAAAAGTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCGTCTGAA 914
          :::|||||||||||||||||||||||||||||||||||||||||||  ||||||
Db   261 ArgThrGlyLysSerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGlu 280

Qy   915 TGTATTACACCAAATGGAAGCATCCCAACGACAAACCATTTCAAAATGTGAACAAAGTT 974
          ||||||||||||||||||||||||||||||||||||||:::|||||||:::
Db   281 CysIleThrProAsnGlySerIleProAsnAspLysProPheGln***GlnAsnValAsnLysIle 300

Qy   975 ACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATG 1034
          ||||||||| ||||:::||||||||||||||||||||||||||:::|||||||||||
Db   301 ThrTyrGlyAlaCysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMet 320

Qy  1035 AGGAATATACCAGAAAAGCAAATCAGA 1061
          ||||||||||:::|||||||||||||
Db   321 ArgAsnValProGluLysGlnThrArg 329


RESULT 13
ABP53897
ID   ABP53897  standard; protein; 329 AA.
XX
AC   ABP53897;
XX
DT   07-JAN-2003  (first entry)
XX
DE   Influenza A virus (A/Bangkok/(H3N2)) haemagglutinin partial protein.
XX
KW   Influenza;Influenza A virus; pathogenicity; RNA viral disease;
KW   viral infection; selenium; vaccine; virucide; anti-HIV.
XX
OS   Influenza A virus.
XX
PN   WO200278717-A2.
XX
PD   10-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-EP003025.
XX
PR   28-MAR-2001; 2001US-00819387.
XX
PA   (NEST ) SOC PROD NESTLE SA.
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Beck M, German B, Levander O, Van Dael P;
XX
DR   WPI; 2002-759948/82.
DR   N-PSDB; ABQ82726.
XX
PT   Treatment of influenza or reducing the risk of contracting influenza
PT   involves administering selenium to an individual.
XX
PS   Example 1; Page; 31pp; English.
XX
CC   The present invention describes a method for treating influenza or
CC   reducing the risk of contracting influenza, which involves administering
CC   selenium to an individual. Also described is a method for enhancing the
CC   efficacy of a viral vaccine by administering an antioxidant, preferably
CC   selenium, to an individual receiving the viral vaccine. The method can be
CC   used for treating influenza, for reducing the risk of contracting
CC   influenza, and for enhancing the efficacy of viral vaccine (preferably
CC   influenza vaccine) in an infant, elderly, a patient or a pet. It can also
CC   be used for treating virus such as coxsackie and HIV virus. The method
CC   provides an improved treatment for viral infection, by reducing in vivo
CC   mutations of the RNA virus. The method also improves a vaccine used to
CC   prevent transmission of an RNA viral disease. The present sequence
CC   represents the haemagglutinin protein from Influenza A virus
CC   (A/Bangkok/(H3N2)). N.B. The present sequence is not given in AF008899,
CC   specification, but is taken from the Genbank accession number AF008899,
CC   as specified on page 7
```

```
CC        efficacy of a viral vaccine by administering an antioxidant, preferably
CC        selenium, to an individual receiving the viral vaccine. The method can be
CC        used for treating influenza. The method for reducing the risk of contracting
CC        influenza, and for enhancing the efficacy of viral vaccine (preferably
CC        influenza vaccine) in an infant, elderly, a patient or a pet. It can also
CC        be used for treating virus such as coxsackie and HIV virus. The method
CC        provides an improved treatment for viral infection, by reducing in vivo
CC        mutations of the RNA virus. The method also improves a vaccine used to
CC        prevent transmission of an RNA viral disease. The present sequence
CC        represents the haemagglutinin protein from Influenza A/Bangkok/
CC        1/79(H3N2). N.B. The present sequence is not given in the specification,
CC        but is taken from the Genbank accession number J02092, as specified on
CC        page 7
XX
SQ        Sequence 550 AA;

Alignment Scores:
Pred.No.:              2.74e-136        Length:               550
Score:                 1449.50          Matches:              262
Percent Similarity:    90.27%           Conservative:          35
Best Local Similarity: 79.64%           Mismatches:            31
Query Match:           75.81%           Indels:                 1
                                        Gaps:                   5

US-10-826-929A-1 (1-1061) x ABP53894 (1-550)

Qy   78  CAAAAC--CCAACCAGTGAAACAACACCACAGCCACATTATGTCTGGGACCACCATGCGAGTA  134
             ||||||  |||||||                  :::   |||::|||||||||||||||||||||
Db    1  GlnAsnLeuProGlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaVal    20

Qy  135  GCAAATGGAACATTGTAAAACAATAACTGATGACCAAATTGAGGTGACAAAATGCTACT  194
             ||||||||||||||||::::||||::|||||||||||||||||||||||||||||||||||
Db   21  ProAsnGlyThrLeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThr    40

Qy  195  GAATTAGTTCAGAGCATTTCAATGGGAAAATATGCAACAACTCATATAAAGTTCTAGAT  254
             ||||||||||||||||||||||||||||||||:::::||||||::||::||||||||||
Db   41  GluLeuValGlnSerSerThrGlyLysTyrIleCysAspSerProHisArgIleLeuAsp    60

Qy  255  GGAGAAAATGCACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAG  314
             |||::||||||||||||||||||||||||||||||||||||||||::|||||||||||||
Db   61  GlyLysAsnCysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGln    80

Qy  315  TATGAGAATTGGGACCTCTTCATAGAAAAGAAGCAGCGCGCTTCAGCAATTGCTACCCATAT  374
             |||  |||||||||||||||||||:::||||||::||||||||||||||||||||||||
Db   81  AsnGluLysTrpAspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyr   100

Qy  375  GACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTC  434
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101  AspValProAspTyrAlaSerLeuArgSerLeuArgSerLeuArgSerGlyThrLeuGluPhe  120

Qy  435  ACAGCAGAGGATTCACATGGACAGTGTCACTCAAAACGAAGAAGTGGAGCCTGCAAA  494
             ||||||||||||||||:::|||||||||||||||||||||::|||||||||||||||||
Db  121  IleAsnGluGlyPheAsnTrpThrGlyValThrGlnSerGlyGlySerTyrAlaCysLys   140

Qy  495  AGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCT  554
             |||||||||  :::|||||||||||||||||||||::::||||||||||||  :::|||
Db  141  ArgGlySerAspAsnSerPhePheSerArgLeuAsnTrpLeuThrGluSerGluSerLys   160

Qy  555  TACCCCACATTGAATGCAAATGCCTAACAATAAAATTCGACAAAACTATACATCTGG  614
             ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db  161  TyrProValLeuAsnValThrMetProAsnGlyAsnPheAspLysLeuTyrIleTrp   180

Qy  615  GGGATTCATCACCCGAGCTCAAACCAACAGCAGAGAATTGTACATCCAAGAAATCAGGA  674
             ||||||||||||||||||||||:::||||||||||||||||:::||||||||||||||||
Db  181  GlyValHisHisProSerThrAspLysGlnGlnThrAsnLeuTyrValArgAlaSerGly  200

Qy  675  CGAGTAACAGTCTCAACAAAAGAGTCAACAAACAGATAGTCCCTAATATCGGATCTAGA  734
             |||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db  201  ArgValThrValSerThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArg  220

Qy  735  CCGTGGGTTAGGGTCAATCAGCCAGGATAAGCATTATACTGACCATTGTAAAACCTGGA  794
             |||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db  221  ProTrpValArgGlyLeuSerGlyArgIleSerArgIleSerIleTyrTrpThrIleValLysProGly  240
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Db  201  HisProSerThrAspLysGluGlnThrAsnLeuTyrValGlnAlaSerGlyLysValThr  220
Qy  684  GTTCAACAAAAGAAGTCAACAAACGAGAGTCCCTAATATCGGATCTAGACCGTGGGTT  743
             |||||||||||||||||||||||||:::||||||||||||
Db  221  ValSerThrLysArgSerArgIleSerArgIleLeuProAsnValGlySerArgProTrpVal  240
Qy  744  AGGGGTCAATCAGCCAGGATAAGCATTATACTGACCAGCATTGTAAAACCTGGAGATATCCTA  803
             |||||||  |||                 |||||||||||||||||||||||||||||
Db  241  ArgGlyLeuSerSerArgIleSerIleTyrTrpTrpThrIleValLysProGlyAspIleLeu  260
Qy  804  ATGATAAACAGTATGGCAACTTAGTTGCACCGCCGGGGATATTTAAATTGAAAACAGGG  863
             ::::||||||||:::|||||||||||||||||||||||||||||||||:::|::::
Db  261  ValIleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetArgThrGly  280
Qy  864  AAAAGCTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAAATGTATTACA  923
             ||||||||||||||||||||:::||||||||||||||||      |||
Db  281  LysSerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThr  300
Qy  924  CCAAATGGAAGCATCCCCAACGACAAAACCATTTCAAAATGTGAACAAAGTTACATATGGA  983
             ||||||||||||||||||||||||||||||||||||||:::|||||||:::||||||||||
Db  301  ProAsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGly  320
Qy  984  AAATGCCCCAAGTATATCCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAAATATA  1043
             ||||||||||||||||::::|||||||||||||||||||||||||||:::|:::
Db  321  AlaCysProLysTyrLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnVal  340
Qy  1044 CCAGAAAGCAAATCAGA  1061
             |||||||||||||||
Db  341  ProGluLysGlnThrArg  346
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RESULT 12
ABP53894
ID   ABP53894 standard; protein; 550 AA.
XX
AC   ABP53894;
XX
DT   07-JAN-2003  (first entry)
XX
DE   Influenza A/Bangkok/1/79 (H3N2), haemagglutinin protein.
XX
KW   Influenza; Influenza A virus; pathogenicity; RNA viral disease;
KW   viral infection; selenium; vaccine; virucide; anti-HIV.
XX
OS   Influenza A virus.
XX
FH                  Key             Location/Qualifiers
FH
FT   Misc-difference 1..550
FT                                  /note= "X is unknown"
XX
PN   WO200278717-A2.
XX
PD   10-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-EP003025.
XX
PR   28-MAR-2001; 2001US-00819387.
XX
PA   (NEST ) SOC PROD NESTLE SA.
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Beck M, German B, Levander O, Van Dael P;
XX
DR   WPI; 2002-759948/82.
DR   N-PSDB; ABQ82723.
XX
PT   Treatment of influenza or reducing the risk of contracting influenza
PT   involves administering selenium to an individual.
XX
PS   Example 1; Page; 31pp; English.
XX
CC   The present invention describes a method for treating influenza or
CC   reducing the risk of contracting influenza, which involves administering
CC   selenium to an individual. Also described is a method for enhancing the
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PR   23-AUG-1982;   82US-00410455.
PR   29-AUG-1983;   83US-00527401.
XX
PA   (SCRI-) SCRIPPS CLINIC & RE.
XX
PI   Green N, Alexander S;
XX
DR   WPI; 1984-062820/10.
XX
PT   Immunogenic peptide(s) contg. 8-40 amino acid residues - useful for
PT   prevention and treatment of influenza.
XX
PS   Disclosure; Fig 1; 45pp; English.
XX
CC   When the peptides of the invention (see FT) are administered, they elicit
CC   the prodn. of antibodies to neutralise more than one strain of influenza
CC   virus and so they are useful for the prevention, diagnosis and treatment
CC   of influenza. (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 386 AA;

     Alignment Scores:
     Pred. No.:                           Length:               386
     Score:                   1472.00     Matches:              270
     Percent Similarity:      87.57%      Conservative:          33
     Best Local Similarity:   78.03%      Mismatches:            41
     Query Match:             76.99%      Indels:                 2
     DB:                                  Gaps:                   2

     US-10-826-929A-1 (1-1061) x AAP40615 (1-386)

Qy    30  ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCAGTCAAAC--CCA    86
              ||     :::            ||||:::|||||||||||||||||||
Db     1  MetLysThrIleIleAlaLeuSerTyrIlePheCysLeuValPheAlaGlnAsnLeuPro    20

Qy    87  ACCAGTGGAAACAAC--ACAGCCACCATTATGTCTCGGACAACCATGCGAGTAGCAAATGGA   143
             :::          |||||||||:::|||||||||||||||||||
Db    21  GlyAsnAspAsnAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGly    40

Qy   144  ACATTGGTAAAAACAATAACTGATGACCAAAATTGAGGTGACAAATGCTACTGAATTAGTT   203
             |||||||||:::||||||||||||||||||:::||||||||||||||||||
Db    41  ThrLeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuVal    60

Qy   204  CAGAGCCATTCAATAGGGAAAATATGCAAACAACTCATATAAGTTCTAGATGGAAGAAAT   263
             ||||||||||            :::::||||||||||||||||:::||||
Db    61  GlnSerSerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyIleAsn    80

Qy   264  TGCACATTAATAGATGACAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAAT   323
             ||||||||:::||||||||||:::||||||||||||||||
Db    81  CysThrLeuIleAspAspAsnAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluLys   100

Qy   324  TGGGACCTCTCATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCT   383
             ||||||||||            :::::||||||||||||||
Db   101  TrpAspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspValPro   120

Qy   384  GACTATGCATCGCTCCGGTCCATTGTAGCATCCTCCAGGAACCATTAGAATTCACAGCAGAG   443
             ||||||||||:::||||||||||||||||||||||
Db   121  AspTyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleAsnGlu   140

Qy   444  GGATTCACCATGGACAGCAGGTGTCACTCAAGAAGACGGAAGAAGTGCAAAAGGGGATCA   503
             ||||||||:::||||||||||||||||:::||||
Db   141  GlyPheAsnTrpThrGlyValThrGlnAsnGlyGlySerSerAlaCysLysArgGlyPro   160

Qy   504  GCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACA   563
             |||||||||:::||||||||||||||||
Db   161  AspSerGlyPhePheSerArgLeuAsnTrpLeuTyrLysSerGlySerThrTyrProVal   180

Qy   564  TTGAATGTGACAATGCTAACAATAAAAATTTCGACAAATATACATCTCGGGGATTCAT   623
             |||||||||:::||||||||||||||||
Db   181  GlnAsnValThrMetProAsnAspAsnSerAspLysLeuTyrIleTrpGlyValHis   200

Qy   624  CACCCGAGCTCAAACCAACCAGCAGCAGAATTGTACATCCAAGAATCAGGACGAGTAACA   683
             ::::::::|||||  |||||
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Qy   687  TCAACAAAAGAAGTCAACAAACAATAGTCCCTAATATCGGATCTTAGACCGTGGGTTAGG   746
             |||||||||:::|||||||||||||||||||
Db   221  SerThrLysArgSerGlnGlnThrValIleProAsnIleGlySerArgProValArg   240

Qy   747  GGTCAATCAGGCAGGATAAGCCATATATACTGACCATTGTAAAACCTGGAGATATCCTAATG   806
             |||  |||   |||||||||||||||||||
Db   241  GlyLeuSerSerArgIleSerIleSerArgTrpThrIleValLysProGlyIleLeuLeu   260

Qy   807  ATAAACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAAAACAGGGAAA   866
             |||||||||:::||||||||||||||||||
Db   261  IleAsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLys   280

Qy   867  AGCTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGTATTACACCA   926
             ||||||||||:::|||||||||||||||||
Db   281  SerSerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThrPro   300

Qy   927  AATGGAAGCATCCCCAACGACAAACCATTCAAAAATGTGAACAAAGTTACATATGGAAAA   986
             |||||||||:::||||||||||||||||||
Db   301  AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla   320

Qy   987  TGCCCCAAGTATATCAGGCAAAACACTTTAAAGTCTGGCCACTGGGATGAGGAATATACCA  1046
             ||||||||||:::|||||||||||||||||
Db   321  CysProLysTyrValLysGlnAsnThrLeuLysSerGlyHisTrpAspGluGluTyrGlyAla   340

Qy  1047  GAAAAGCAAATCAGA  1061
             ||||||||||
Db   341  GluLysGlnThrArg   345
```

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RESULT 11
AAP40615
ID   AAP40615 standard; protein; 386 AA.
XX
AC   AAP40615;
XX
DT   24-OCT-2003  (revised)
DT   12-FEB-1992  (first entry)
XX
DE   Sequence of the X-47 haemagglutinin (HA) molecule contg. the entire HA1
DE   and the amino-terminus of HA2.
XX
KW   Vaccine; immunogen; antigen; diagnosis; therapy; influenza; virus.
XX
OS   Influenza A virus; (H3N2).
XX
FH   Key                 Location/Qualifiers
FT   Protein             17..346
FT                       /label= HA1
FT   Peptide             69..76
FT                       /note= "claimed"
FT   Peptide             155..176
FT                       /note= "claimed"
FT   Peptide             294..319
FT                       /note= "claimed"
FT   Peptide             294..313
FT                       /note= "claimed"
FT   Peptide             322..346
FT                       /note= "claimed"
FT   Peptide             342..351
FT                       /note= "claimed"
FT   Peptide             346..374
FT                       /note= "claimed"
FT   Protein             347..386
FT                       /label= HA2
FT   Peptide             347..374
FT                       /note= "claimed"
XX
PN   WO8400687-A.
XX
PD   01-MAR-1984.
XX
PF   23-AUG-1983;  83WO-US001291.
XX
```

XX
CC   The present invention describes a method for treating influenza or
CC   reducing the risk of contracting influenza, which involves administering
CC   selenium to an individual. Also described is a method for enhancing the
CC   efficacy of a viral vaccine by administering an antioxidant, preferably
CC   selenium, to an individual receiving the viral vaccine. The method can be
CC   used for treating influenza, for reducing the risk of contracting
CC   influenza, and for enhancing the efficacy of viral vaccine (preferably
CC   influenza vaccine) in an infant, elderly, a patient or a pet. It can also
CC   be used for treating virus such as coxsackie and HIV virus. The method
CC   provides an improved treatment for viral infection, by reducing in vivo
CC   mutations of the RNA virus. The method also improves a vaccine used to
CC   prevent transmission of an RNA viral disease. The present sequence
CC   represents the haemagglutinin protein from Influenza A virus
CC   (A/Bangkok/1/79). N.B. The present sequence is not given in the
CC   specification, but is taken from the Genbank accession number AF201843,
CC   as specified on page 7
XX
SQ   Sequence 363 AA;

Alignment Scores:
Pred. No.:   Length: 363
Score: 5.83e-139   Matches: 268
Percent Similarity: 1475.50   Conservative: 38
Best Local Similarity: 88.70%   Mismatches: 38
Query Match: 77.68%   Indels: 1
DB: 77.17%   Gaps: 1
                         5

US-10-826-929A-1 (1-1061) x ABP53895 (1-363)

Qy   30 ATGAGAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTACAGTCAAAC--CCA   86
             ||||||| || ||| ||| ||:::|||||| ||:::||
Db   1 MetLysThrIleIleAlaLeuSerTyrIleLeuCysLeuValPheAlaGlnAsnLeuPro   20

Qy   87 ACCAGTGGAACAACACAGCCACCATTATCTCGGACACCATGCAGTAGACAAATGGAACA   146
             ||| ||| ||:::|||||||| |||||||| :::||||||:::||
Db   21 GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThr   40

Qy   147 TTGGTAAAAACAATAACTGACGATGACCAAAATGAGGTGACAAATGCTACTGAATTAGTTCAG   206
             ||||||:::|||||| ||||||||:::||||||||||||||| |||||||||||
Db   41 LeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGln   60

Qy   207 AGCATTTCAATAGGGGAAAATGCAACAACTCATATAAAGTTCAGATGGAAGAAATGCA   266
             ||| ||| :::||||||:::|| :::||||||||||:::||||||||
Db   61 SerSerSerThrGlyArgIleCysAspSerProHisArgIleLeuSerGluCysIleThr   80

Qy   267 ACATTAATAGATGACAATGCTAGGAGACACCCCACTGTGATGTCTTCCAGTATGAGAATTGG   326
             ||||||||:::||||||| ||||||||||:::||||||||| |||||||||||||
Db   81 ThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyGluCysTyrProGlyTrp   100

Qy   327 GACCTCTTCATAGAAGAGCAGCAGCCGCTTTCAGCAATTGCTACCACCATATGACATCCCTGAC   386
             |||||||:::|||||||| |||||||||||||||| |||||||:::||||||||
Db   101 AspLeuPheValGluArgSerLysAlaPheSerAlaIleAlaThrThrProTyrProAsp   120

Qy   387 TATGCATCGTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGGAGGGA   446
             |||||||| |||||||:::||||||||| ||||||||||||| ||||||||||||
Db   121 TyrAlaSerLeuArgSerLeuArgLeuValAlaSerGlyThrLeuGluPheIleAsnGluGly   140

Qy   447 TTCACATGGACAGGTGTCACTCAAAACGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCC   506
             ||||||||| ||:::|||||||||| ||||||||| ||:::|||||||||||
Db   141 PheAsnTrpThrGlyValThrGlnSerGlyGlySerTyrAlaCysLysArgGlySerAsp   160

Qy   507 GATAGTTTCTTAGCCGACTGAATTGGCTAACAACAAATCTGAAACTCTTACCCCACATTG   566
             |||||||:::||||||||| ||||||||||| :::||| :::||||||
Db   161 LysSerPheSerArgLeuAsnTrpLeuTyrGluSerGluSerLysTyrProValLeu   180

Qy   567 AATGTGACAATGCCTAACATTAACATAAAAATTTCGACAACTATACATCTGGGGGATTCATCAC   626
             |||||||||||| ||||||||||| ||||||||| :::|||||||||||
Db   181 AsnValThrMetProAsnGlyAsnGlyAsnPheAspValLeuTrpIleLeuTrpIleGlyValHisHis   200

Qy   627 CCGAGCTCAAACCAACAGCACAGACAGAAATTGTACATCCAAGAATCAGGACGAGTAACAGTC   686
             |||||||| :::|||||||||||||| ||||||||||:::|||||||||||:::
Db   201 ProSerThrAspLysGlyGlnThrGluGlnThrArgLeuTyrValArgAlaSerGlyArgValThrVal   220

XX
PT   New nucleic acid molecule binding a polypeptide participating in
PT   influenza virus infection, useful for diagnosing or treating influenza
PT   virus infection in vertebrates such as avian, swines and humans.
XX
PS   Claim 5; SEQ ID NO 1; 121pp; English.
XX
CC   The present sequence is that of influenza virus haemagglutinin.
CC   Oligonucleotides (e.g. aptamers) designed to bind conserved sequences in
CC   the HA polypeptide can be used to prevent virus binding to host cells.
CC   Such aptamers can be used to diagnose and treat influenza virus infection
CC   in vertebrates such as avian, swine and humans. They exhibit viral cross-
CC   reactivity and as such can be used as universal vaccines against the
CC   influenza virus. A claimed nucleic acid molecule comprises a
CC   polynucleotide sequence capable of specifically binding a polypeptide
CC   participating in influenza virus infection of cells. The polypeptide is
CC   an influenza virus polypeptide such as HA or a host cell polypeptide such
CC   as a sialic acid receptor. The nucleic acid molecule is single-stranded
CC   DNA or RNA, e.g. A21 ADR89581 or A22 ADR89582. It is preferably capable
CC   of binding to amino acids 91-261 of the present HA sequence. A claimed
CC   method of generating a molecule capable of inhibiting influenza virus
CC   infection comprises: contacting a plurality of nucleic acid molecules
CC   with a polypeptide participating in influenza virus infection of cells,
CC   e.g. HA; and identifying nucleic acid molecule(s) capable of specifically
CC   binding the polypeptide. The nucleic acid is used in claimed methods of:
CC   treating or preventing influenza virus infection; identifying influenza
CC   virus in a biological sample; and targeting an antiviral agent to an
CC   influenza virus-infected tissue. A claimed polypeptide useful for
CC   vaccination against influenza virus comprises amino acids 91-261, 116-261
CC   or 116-245 of the present HA sequence.
XX
SQ   Sequence 329 AA;

Alignment Scores:
Pred. No.:   329
Score: 9.86e-141   Matches: 268
Percent Similarity: 1493.00   Conservative: 28
Best Local Similarity: 90.80%   Mismatches: 30
Query Match: 82.21%   Indels: 0
DB: 78.09%   Gaps: 0
                            8

US-10-826-929A-1 (1-1061) x ADR89571 (1-329)

```
Qy    84 CCAACCAGTGGAAACAACAACAGCCACATTATGTCTGGACACATGCAGTAGCAAATGGA 143
         ||||||  :||| ||| || ||  || :::||||     ||||| ||| ||||||||
Db     4 ProGlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGly 23

Qy   144 ACATTGGTAAAAACAATAACATGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTT 203
         |||||||||||||:::||||||||||||||||||||||||||||:::||||||||||
Db    24 ThrLeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuVal 43

Qy   204 CAGAGACATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTTAGATGGAAGAAT 263
         ||||| || |||||||:::|||||||   :::::||:|||||:::||||||||
Db    44 GlnSerSerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyIleAsn 63

Qy   264 TGCACATTAATAGATGGCAATGCTAGGAGACCCCACTGTGATGTCTTCCAGTATGAGAAT 323
         |||| |||||||||| ||||||||||||||||||||||||||:::||||||||||||
Db    64 CysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspGlyPheGlnAsnGluThr 83

Qy   324 TGGGACCCTCTTCATAGAAAGAAGAAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCT 383
         |||||||||||||||:::|||||||||:::||||||||
Db    84 TrpAspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspValPro 103

Qy   384 GACTATGCATCGTCCGGTCCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGCAG 443
         ||||||||||||||:::||||||||||||||||||:::||||||||||||
Db   104 AspTyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheAsnGlu 123

Qy   444 GGATTCACATGGACAGGTGTCACTCAAAACGAAGAAGTGGAGCCTGCAAAAGGGGATCA 503
         ||||||||||||||||||:::||||||||||||||||||||
Db   124 GlyPheThrTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyPro 143

Qy   504 GCCGATAGTTTCTTAGCCAGACTGAATTGGCTAACAAAATCTGGAAACTTTACCCCCACA 563
         |||||||||||||||:::::|||||
```

Db   181 AsnValThrMetProAsnAsnAspAsnPheAspLysLeuTyrIleTrpGlyValHisHis 200
         |||||||||||||||||||||||||||||||||||||||||||||||
Qy   627 CCGAGCTCAAACCAACCACAGCAGCAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTC 686
         |||||:::::|||||:::||||| ||||||||:||:||
Db   201 ProSerThrAspGlnGluGlnThrSerLeuTyrValGlnAlaSerGlyArgValThrVal 220

Qy   687 TCAACAAAAGAAGTCAACAAACGATAGTCCCTAATATCGGATCCTAGACCGTGGGTTAGG 746
         ||||||||||||||||||||||||:::||||||||||||||:||
Db   221 SerThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArg 240

Qy   747 GGTCAATCAGGCAGGATAAGCATATATACTGACCATTGTAAAACCTGGAGATATCCTAATG 806
         ||| ||||||||:::::|||||||||||||||:|||||:::
Db   241 GlyLeuSerSerArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuVal 260

Qy   807 ATAAACAGTAATGGCAACTTAGTTGCACCGCGGGGGATATTTAAATTGAAAACAGGGAAA 866
         ||||||||||:::||||||||||||||||||||:::::|||||
Db   261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetArgThrGlyLys 280

Qy   867 AGCCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAAATGTATTACACCA 926
         |||||||:||:::|||||||||||||||||||||||:||||||
Db   281 SerSerIleMetArgSerAspAlaProIleGlyTyrCysIleSerGluCysIleThrPro 300

Qy   927 AATGGAAGCATCCCCAACGACAACAAACCATTCAAAATGTGAACAAGTTACATATGGAAAA 986
         |||||||||||||:::|||||||||||||||||||||||||||:||
Db   301 AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla 320

Qy   987 TGCCCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCA 1046
         |||||||||||:::::|||||||:::::|||||||||||||:::::||
Db   321 CysProLysTyrValLysGlnAsnThrLeuAsnThrLeuLeuAlaThrGlyMetArgAsnValPro 340

Qy 1047 GAAAAGCAAATCAGA 1061
         |||||||||||||
Db   341 GluLysGlnThrArg 345

RESULT 9
ADR89571
ID   ADR89571 standard; protein; 329 AA.
XX
AC   ADR89571;
XX
DT   02-DEC-2004 (first entry)
XX
DE   Influenza virus haemagglutinin.
XX
KW   Haemagglutinin; aptamer; vaccine; gene therapy; DNA immunisation;
KW   virucide.
XX
OS   Influenza virus.
XX
FH   Key   Location/Qualifiers
FH
FT   Region   91..261
FT   /note= "Region specifically referred to in Claim 105"
FT   Region   116..261
FT   /note= "Globular region, mediates binding to host cell
FT   determinants; this region is specifically referred to in
FT   Claim 106"
FT   Region   116..245
FT   /note= "Region specifically referred to in Claim 107"
XX
PN   WO2004076621-A2.
XX
PD   10-SEP-2004.
XX
PF   24-FEB-2004; 2004WO-IL000182.
XX
PR   27-FEB-2003; 2003US-0449863P.
XX
PA   (YEDA) YEDA RES & DEV CO LTD.
XX
PI   Arnon R, Jeon S, Kayhan B, Ben-Yedidya T;
XX
DR   WPI; 2004-653392/63.

```
XX
DR   WPI; 2002-139923/18.
DR   N-PSDB; ABA93944.
XX
PT   Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
PT   polypeptide, useful in diagnosis and for generating new influenza A
PT   variant strains.
XX
PS   Disclosure; Page 83-85; 103pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) having the
CC   complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
CC   strand, antigenomic message sense. ABA93934 to ABA93944 encode the
CC   Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774
CC   from the present invention. (I) is useful for designing polymerase chain
CC   reaction (PCR) primers for use in a PCR assay to detect the presence of
CC   the corresponding virus segment in a sample or for designing and
CC   selecting peptides for use in an enzyme linked immunosorbant assay to
CC   detect the presence of the corresponding protein produced by that segment
CC   in a sample, hence is useful in diagnosis and may be modified by mutation
CC   to generate new Influenza A variant strains. ABA94945 to ABA94039
CC   represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
CC   are used in an example from the present invention
XX
SQ   Sequence 566 AA;

Alignment Scores:
Pred. No.:                                  Length:          566
Score:                  1502.50             Matches:         274
Percent Similarity:     88.70%              Conservative:    32
Best Local Similarity:  79.42%              Mismatches:      38
Query Match:            78.58%              Indels:          1
DB:                     5                   Gaps:            1

US-10-826-929A-1 (1-1061) x ABB05774 (1-566)

Qy   30 ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTACAGTCAAAAC---CCA   86
         ||||||||   |||||||||:|| ||||||  ||| |||||||  |||::  :|||   :||
Db    1 MetLysThrIleIleLeuSerTyrIlePheCysLeuValLeuGlyGlnAspPhePro     20

Qy   87 ACCAGTGGAACACACAGCCACCATTATGTCTGGGACACCATGCAGTAGCAAATGGAACA  146
         :: |||||||||||||||| |||||||| :||| |||||||||||||||||||||||
Db   21 GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThr   40

Qy  147 TTGGTAAAACAATAACTGATGACCAAAATGGACAAAATGCTACTGAATTAGTTCAG      206
         ||||||||||||||||:||:||||||||:||||||||||||||||||||||||||
Db   41 LeuValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGln   60

Qy  207 AGCATTCAATAGGGAAAATATGCCAACAACTCATATAAAGTTCAGATGGAAGAAATGC    266
         ||| |||||||||||||||||||| :::::::::||||||||||||||||||||||
Db   61 SerSerSerThrGlyLysLysCysAsnAsnProHisArgIleLeuAspPheCys        80

Qy  267 ACATTAATGATGCAATGCAATGGTAGGAGACACCCCACTGTGATGTCTTCCAGTATGAGAATTGG  326
         ||||||||||| |||||||||||||:::  |||||||||||||||||||||||||||||||||
Db   81 ThrLeuIleAspAlaThrLeuAsnGlyGlyAspProHisCysAspGlyPheGlnAsnGluThrTrp  100

Qy  327 GACCTCTTCATAGAGAAGAGACAGCGCCTTTCAGCAATTGCTACCACCATATGACATCCCTGAC  386
         |||||||||:::|||||||||||||||||||||||||||||||||||:::|||||||||||||
Db  101 AspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspValProAsp      120

Qy  387 TATGCATCGTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGA     446
         ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db  121 TyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleSerGluGly    140

Qy  447 TTCACATGGACAGGTGTCACTCAAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCC    506
         |||||||||||||||||||||:::|||||||||||||||||||||||||||||||:::|||
Db  141 PheThrTrpThrGlyValThrGlnAsnGlyLysSerAsnAlaCysLysArgGlyProAsp    160

Qy  507 GATAGTTCTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTG             566
         ||||||||||||||||||||||:::::||||||||||||||||||||||
Db  161 SerGlyPhePheSerArgLeuAsnTrpLeuTyrLysSerGlyTyrProValLeu        180

Qy  557 AATGTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGGATTCATCAC    626
         ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db  181 AsnValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyValHisHis    200

Qy  627 CCGAGCTCAAACCAACCACAGCAGCAGAATTGTACATCCAAGAATCAGAGCGAGTAACAGTC  686
         ||||||::||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db  201 ProSerThrAspGlnGluGlnThrSerLeuTyrValGlnAlaSerGlyArgValThrVal    220

Qy  687 TCAACAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGG     746
         |||||||||:::|||||||||||||||||:::||||||||||||||||||||||||||
Db  221 SerThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArg   240

Qy  747 GGTCAATCAGGCAGGATAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATG    806
         ||:::|||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db  241 GlyLeuSerSerArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuVal   260

Qy  807 ATAAACAGTAATGCCAACTTAGTTGCACCGCGGGGGATATTTAAATTGAAAACAGGGAAA   866
         |||||||||||||||:::|||||||||||||||||:::|||||||||||||||||||||
Db  261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetArgThrGlyLys   280

Qy  867 AGTCTGTAATGAAGATCAGACGCCCCATAGACATGCACCATTGTGTGTCTGAATGTATTACCA   926
         |||||:::|||||||||||||||:::|||||||||||||||||||||||||:::|||||||
Db  281 SerSerIleMetArgSerAspAlaProIleGlyThrCysIleSerGluCysIleThrPro    300

Qy  927 AATGGAAGCACCCCAACGACACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAA    986
         |||||||||||||||||||||||:::|||||||||||||||:::|||||||||||||
Db  301 AsnGlySerIleProGluProAsnAspLysProPheGlnAsnValAsnValIleThrTyrGlyAla  320

Qy  987 TGCCCCAAGTATATCAGGCAAAACACTTAAAGCTGCCACTGGCCATGGGATGGAGAATATACCA 1046
         ||||||||||||||||||:::|||||||||||||||||||||:::|||||||||||||||||
Db  321 CysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValPro     340

Qy 1047 GAAAAGCAAATCAGA 1061
         |||||||||||||
Db  341 GluLysGlnThrArg 345
```

RESULT 8
ABB05774

```
ID   ABB05774 standard; protein; 566 AA.
XX
AC   ABB05774;
XX
DT   07-MAY-2002 (first entry)
XX
DE   Influenza A/Udorn/72 (H3N2) Strain HA protein SEQ ID NO:22.
XX
KW   Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
KW   Influenza A virus; genome.
XX
OS   Influenzavirus A.
XX
PN   WO200200884-A2.
XX
PD   03-JAN-2002.
XX
PF   21-JUN-2001; 2001WO-US019826.
XX
PR   23-JUN-2000; 2000US-0213650P.
XX
PA   (AMCY ) AMERICAN CYANAMID CO.
XX
PI   Galarza JM, Latham TE;
```

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Db        |||   |||     |||||||||||||   :::::::::||||||||    :::|||
          61  SerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyIleAspCys   80

Qy   267  ACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGCTTCCAGTAGCAAATGGAACA   326
          ||||||||||||||||  :::|||||||||||||  ||||||||||||||||||||||
Db    81  ThrLeuIleAspAlaLeuLeuLeuGlyAspProHisCysAspValPheGlnAsnGluThrTrp   100

Qy   327  GACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGAC   386
          ||||||||||::|||||||||||||::||||||||||||||||:::||||||||||
Db   101  AspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspValProAsp   120

Qy   387  TATGCATCGTCCCGTCCATTGTGACATCCTCAGGAACATTAGAATTCACAGCAGAGGGA   446
          ||||||||||||||::|||||||||  |||  |||||||||::||||||||||||||
Db   121  TyrAlaSerLeuArgSerLeuValAlaSerGlyThrLeuGluPheIleThrGluGly   140

Qy   447  TTCACAATGGACAGGTGTCACTCAAAACGGAGAAGAGCCTGCAAAGGGGGATCAGCC   506
          |||||||||||||||  |||  |||||||||||  ||||:::|||||||||||||
Db   141  PheThrTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyProGly   160

Qy   507  GATAGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACCATTG   566
          |||||||||||||||||||||||||||  ||||||||:::|||||||||
Db   161  SerGlyPhePheSerArgLeuAsnTrpLeuThrLysSerTyrProValLeu   180

Qy   567  AATGTGACAATGCCTAACACATAAAAATTCGACAAACTTACATCTGGGGGATTCATCAC   626
          ||||||||||||||||||||  |||||||  :::|||||||||||||||||||||||
Db   181  AsnValThrMetProAsnAsnAspAsnPheAspLysLeuTyrIleTrpGlyIleHisHis   200

Qy   627  CCGAGCTCAAACCACCACAGCAGCAGAATTGTACATCCAAGAATCAGGAGCCAGTAACAGTC   686
          |||||||::|||||||||||||  ||||||  ||||||||||||||||||||||||||
Db   201  ProSerThrAsnGlnGluGlnThrSerLeuTyrValGlnAlaSerGlyArgValThrVal   220

Qy   687  TAACAAAAGAAGTCAACAAACGATAGTCCCTATATCGGATCTAGACCGTGGTTAGG   746
          |||:::|||||||||||||||  |||:::||||||  :::|||||||||||||||||
Db   221  SerThrArgArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArg   240

Qy   747  GGTCAATCAGGCAGGATAAGCAGCATAATGACTGACCATTGTAAAACCTGGAGATATCCTAATG   806
          |||||||||:::|||:::||:::||||||||||||||:::||||:::|||:|:||
Db   241  GlyLeuSerSerArgIleSerArgIleTyrArgTrpThrIleValLysProGlyAspValLeuVal   260

Qy   807  ATAAACAGTAATGGCAACTTAGTTGCACCCGGGGATATTTTAAATTGAAAACAGGGAAA   866
          ||||||||||||||||||||:::||||:::||||||:::|||||:::::||||||||
Db   261  IleAsnSerAsnGlyAsnLeuLeuIleAlaProGlyAspIleTyrPheLysMetArgThrGlyLys   280

Qy   867  AGCTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAAATGTATTACACCA   926
          ||||||||||||:::|||:||||||||||||:::||||||||||||||||||||||
Db   281  SerSerIleMetArgSerArgAspAlaProIleAspIleCysValSerGluCysIleThrPro   300

Qy   927  AATGGAAGCATCCCCAACGGACAAACCATTCAAAATGTGAACAAAGTTACATGGGAAAA   986
          ||||||||||||||||||||  |||||||||||:::||||||:::|||||||||
Db   301  AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla   320

Qy   987  TGCCCCAAGTATATCAGGCAAAACACTTTAAAGCTGCCGGATGAGGAATATACCA   1046
          ||||||||||||||:::::|||||||||||||||||||||:::|||||||||
Db   321  CysProLysTyrValLysGlnAsnThrLeuLysLeuLeuAlaThrGlyMetArgAsnValPro   340

Qy  1047  GAAAAGCAAATCAGA   1061
          |||||||||||||
Db   341  GluLysGlnThrArg   345
```

RESULT 7
ABB05767
ID   ABB05767 standard; protein; 566 AA.
XX
AC   ABB05767;
XX
DT   07-MAY-2002 (first entry)
XX
DE   Influenza A/Udorn/72 (H3N2) Strain HA protein SEQ ID NO:8.
XX
KW   Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
KW   Influenza A virus; genome.
XX
OS   Influenzavirus A.

PT   Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
PT   polypeptide, useful in diagnosis and for generating new influenza A
PT   variant strains.
XX
PS   Claim 19; Page 64-65; 103pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) having the
CC   complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
CC   strand, antigenomic message sense. ABA93934 to ABA93944 encode the
CC   Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774
CC   from the present invention. (I) is useful for designing polymerase chain
CC   reaction (PCR) primers for use in a PCR assay to detect the presence of
CC   the corresponding virus segment in a sample or for designing and
CC   selecting peptides for use in an enzyme linked immunosorbant assay to
CC   detect the presence of the corresponding protein produced by that segment
CC   in a sample, hence is useful in diagnosis and may be modified by mutation
CC   to generate new influenza A variant strains. ABA94945 to ABA94039
CC   represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
CC   are used in an example from the present invention
XX
SQ   Sequence 566 AA;

Alignment Scores:
Pred. No.:   Length: 566
Score: 4.12e-142   Matches: 275
Percent Similarity: 88.70%   Conservative: 31
Best Local Similarity: 79.71%   Mismatches: 38
Query Match: 78.84%   Indels: 1
DB: 5   Gaps: 1

US-10-826-929A-1 (1-1061) x ABB05767 (1-566)

```
Qy    30  ATGAGACAACCATTATTTTGATACTACTGACCCATTGGTGCTCACAGTCAAAAC---CCA   86
          |||||||||  |||||||||||||||||||||||||||||| :::
Db     1  MetLysThrIleIleAlaLeuSerTyrIlePheCysLeuValLeuGlyGlnAsnPhePro   20

Qy    87  ACCAGTGGAAACAACAGCCTAGGAGACCCCCACTGTGCTGGGACACCATGCAGTAGCAAATGGAACA   146
          ||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db    21  GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThr   40

Qy   147  TTGGTAAAACAATAACTACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAG   206
          ||||||||||||||:::|||||||  |||:::|||||||||||||||||||||||||
Db    41  LeuValLysThrThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGln   60

Qy   207  AGCATTCAATAGGAGAAAATATGCAACAACTCATATAAAGTTCTAGATGCGATGAAGAATTGC   266
          ||||||||||||||||||||||||    :::::|||||||||||||||:::||||
Db    61  SerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyIleAspCys   80

Qy   267  ACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGCTTCCAGTAGCAAATGGAACA   326
          |||||||||||||||:::|||||||||||||  |||||||||||||||||||||||||
Db    81  ThrLeuIleAspAlaLeuLeuLeuGlyAspProHisCysAspValPheGlnAsnGluThrTrp   100

Qy   327  GACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCATATGACATCCCTGAC   386
          |||||||||::|||||||||||||||||||||||||||||:::||||||||||||||
Db   101  AspLeuPheValGluArgSerLysAlaPheSerAsnCysTyrProTyrAspVallProAsp   120

Qy   387  TATGCATCGTCCCGGTCCATTGTGAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGA   446
```

FT   Domain   17..70
FT   /note= "Stem region in N-terminal domain"
FT   Domain   71..289
FT   /note= "Globular head domain"
FT   Domain   290..566
FT   /note= "Stem region in C-terminal domain"
FT   Peptide   334..338
FT   /note= "Conserved region A""
FT   Peptide   392..403
FT   /note= "Conserved region B""
PN   EP61339-A2.
XX
PD   26-OCT-1994.
XX
PF   20-APR-1994; 94BP-00302819.
XX
PR   20-APR-1993; 93JP-00115216.
PR   16-MAR-1994; 94JP-00070194.
XX
PA   (TAKI) TAKARA SHUZO CO LTD.
XX
PI   Okuno Y, Isegawa Y, Sasao P, Ueda S;
XX
DR   WPI; 1994-325949/41.
DR   N-PSDB; AAQ72855.
XX
PT   Human influenza-A virus haemagglutinin polypeptide(s) - useful in
PT   influenza-A vaccine composition;
XX
PS   Example 2; Page 54-58; 68pp; English.
XX
CC   The cDNA encoding this sequence was amplified using the primer sequences
CC   given in AAQ72852-54 and this sequence represents the full length
CC   hemagglutinin (HA) protein gene of the H3N2 subtype of human influenza A
CC   virus, strain A2/Aichi/2/68. This full length protein contains two
CC   conserved regions, the A' region, TGMRN and the B region,
CC   QINGKLNR(L/V)IEK. These regions are close to each other in the stem of
CC   the HA molecule and they represent epitopes which are recognised by the
CC   antibody C179. C179 binds to the stem region of the HA molecule and thus
CC   inhibits the membrane fusion action of the HA molecule and neutralises
CC   the virus. Polypeptide molecules which contain the conserved peptide
CC   regions, A and B, esp. HA molecules lacking the globular head region (see
CC   also AAR63591), are antigenically equivalent to the stem region of the HA
CC   molecule of influenza A virus. These artificial peptides may be used as
CC   vaccines for prophylaxis of influenza A virus infection. (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 566 AA;

Alignment Scores:
Pred. No.:   Length: 566
Score: 4.04e-144   Matches: 277
Percent Similarity: 1527.50   Conservative: 30
Best Local Similarity: 88.99%   Mismatches: 37
Query Match: 80.23%   Indels: 1
DB: 79.89%   Gaps: 1
                            2

US-10-826-929A-1 (1-1061) x AAR63590 (1-566)

Qy   30   ATGAGAGACAACCATTATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAAC---CCA   86
          ||||||||| ||| |::: ||||::: |||||
Db   1   MetLysThrIleIleAlaLeuSerTyrIlePheCysLeuAlaLeuGlyGlnAspLeuPro   20

Qy   87   ACCATTGGAACAACACAGCCACCATTATGTCTGGGACACCATGCAGTAGCAAATGAACA   146
          ||| ||| ||:||:|| |||| |||||||| |||||||||
Db   21   GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThr   40

Qy 147   TTGGTAAAAACAATAACTGATGACCAAAATGAGGTGACAAATGCTACTGAATTAGTTCAG   206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41   LeuValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGln   60

Qy 207   AGCATTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTTCTGATGGAAGAAATTGC   266

```
Db    41  ValLysThrThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer  60

Qy   210  ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA  269
              ||||||||||||| ||:::|| |||||||||||||||| ||||||
Db    61  ThrSerIleGlyLysIleCysAsnAsnProTyrArgValLeuAspGlyArgLysCysThr  80

Qy   270  TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC  329
              ||||||||||||||||||||||||||||||||||||||||||||||
Db    81  LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp  100

Qy   330  CTCTTCATAGAAAAGAAGCAGCGCTTCAGCAATTGCTACCCATATGACATCCCTGACTAT  389
              ||||||||||||||||||||||||||||||||||||||||:::||||
Db   101  LeuPheIleGluLysLysGlnArgPheSerAsnCysTyrProTyrAspIleProAspTyr  120

Qy   390  GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC  449
              ||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe  140

Qy   450  ACATGACAGGTGTCACTCAAAACGAAGAGTGGAGCCTGCAAAAGGGATCAGCCGAT  509
              ||||||||||||||||||||||||||:::||||||||||||||
Db   141  ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysArgArgGlySerAlaAsp  160

Qy   510  AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT  569
              ||||||||||||||||||||||||||||||||||||||||||:::||||
Db   161  SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn  180

Qy   570  GTGACAATGCCTAACAATAAAAATTTCGACAACTATACATCTGGGGATTCATCACCCG  629
              ||||||||||||||||||||||||||||||||||||||||||||
Db   181  ValThrMetProAsnAsnAsnAsnPheAspAsnTyrIleTyrIleTrpGlyIleHisHisPro  200

Qy   630  AGCTCAAACCACACAGCAGAGAATTGTACATCCAAGAATCAGGAGACGAGTAACAGTCTCA  689
              |||:::||  ||:::||||||||| ||||||||||||
Db   201  SerThrAsnAsnGluGlnThrLysGluTyrIleGlnGluSerGlyAspGluValThrValSer  220

Qy   690  ACAAAAAGAAGTCAACAACAGATAGTCCCTAATATCGGATCCAGACCGTGGGTTAGGGGT  749
              ||:::|||||||||||||||||||||||||||||||||||||||
Db   221  ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProValArgGly  240

Qy   750  CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA  809
              ||||||||||||||||||||||||||||||||||||||||||||
Db   241  GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle  260

Qy   810  AACAGTAATGGCAACTTAGTTGCACCCGGGGATATTTTAAATTGAAACAGGAAAAGC  869
              |||||||||||||||||||||:::|||||||||||||
Db   261  AsnSerAsnGlyAsnLeuValAlaArgArgGlyTyrPheLysMetArgThrGlyLysSer  280

Qy   870  TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTACACCAAAT  929
              ||||||||||||||||||||||||||||||:::||||||||
Db   281  SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn  300

Qy   930  GGAAGGCATCCCCAACAACAACACCATTTCAAAATGTGAACAAAGTTACATATGGAAATGC  989
              ||||||||||||||||||||||||||||||||||||||||||||
Db   301  GlySerIleProAsnAspAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys  320

Qy   990  CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGGAGAATATACCAGAA  1049
              |||:::||||||||||||||||:::|||||||||||||
Db   321  ProLysTyrIleLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu  340

Qy  1050  AAGCAAATCAGA  1061
              ||||||||||||
Db   341  LysGlnIleIleArg  344
```

RESULT 5
AAW44946
```
ID   AAW44946    standard; protein; 565 AA.
XX
AC   AAW44946;
XX
DT   28-OCT-1998  (first entry)
XX
DE   EIV Fontainebleau strain haemagglutinin protein.
XX
KW   Multivalent vaccine; horse; pathogen; respiratory disease; EHV; EIV;
```

```
KW   Clostridium tetani; Borrelia burgdorferi; equine influenza virus; EEEV;
KW   Eastern equine encephalomyelitis virus; equine herpesvirus; WEEV; VEEV;
KW   Western equine encephalomyelitis virus; digestive disease; rabies virus;
KW   Venezuelan equine encephalomyelitis virus; vector; primer; PCR;
KW   amplification; haemagglutinin.
XX
OS   Equine influenza virus.
XX
PN   FR2751226-A1.
XX
PD   23-JAN-1998.
XX
PF   19-JUL-1996;   96FR-00009400.
XX
PR   19-JUL-1996;   96FR-00009400.
XX
PA   (INMR ) RHONE MERIEUX SA.
XX
PI   Audonnet JCF, Bouchardon A, Riviere MEA;
XX
DR   WPI; 1998-112826/11.
DR   N-PSDB; AAV49391.
XX
PT   Multi-valent polynucleotide vaccines against equine pathogens - consist
PT   of at least 3 plasmids able to express protective antigens from specified
PT   viruses.
XX
PS   Example 14; Fig 8; 49pp; French.
XX
CC   The invention relates to a multivalent vaccine for protecting horses
CC   against several pathogens, especially pathogens associated with
CC   respiratory and digestive diseases. The pathogens are especially selected
CC   from equine herpesvirus (EHV), equine influenza virus (EIV), Clostridium
CC   tetani, Borrelia burgdorferi, Eastern, Western or Venezuelan equine
CC   encephalomyelitis viruses (EEEV, WEEV and VEEV, respectively) and rabies
CC   virus. The vaccines are preferably composed of polynucleotide sequences
CC   encoding 3 antigens, all as part of vectors. This sequence represents the
CC   EIV Fontainebleau strain haemagglutinin protein. The coding sequence was
CC   subcloned into the plasmid pVR1012 to generate plasmid pAB099 for use in
CC   the vaccine
XX
SQ   Sequence 565 AA;
XX
```

Alignment Scores:
```
Pred. No.:                              Length:         565
Score:               1.78e-167          Matches:        324
                     1760.00            Conservative:    13
Percent Similarity:  97.97%             Mismatches:       7
Best Local Similarity: 94.19%           Indels:           0
Query Match:         92.05%             Gaps:             0
DB:                  2
```

US-10-826-929A-1 (1-1061) x AAW44946 (1-565)

```
Qy    30  ATGAAGACAACAATAACTGATGACCATTATTTGATACTACTGACCCTCTGGGTCTCACAGTCTCAAAACCCAACC  89
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MetLysThrThrIleThrAspAspHisTyrLeuIleLeuLeuThrLeuTrpValTyrSerGlnAsnProThr  20

Qy    90  AGTGGAAACAACAACAGCCACATTATGTCTGGACACCAGTAGCAAATGGAACATTG  149
              ||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db    21  SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu  40

Qy   150  GTAAAAACAATAACTGATGACCATTATTTGATACTACTGACCCTCTGGGTCTCACAGTCTCAAAACCCAACC  89
```

DB: 2   Gaps: 0

US-10-826-929A-1 (1-1061) x AAR04943 (1-565)

```
Qy      30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGTCTACAGTCAAAACCCAACC 89
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy      90 AGTGGAAACAACACAGCCACCATTATGTCTGGGACACCATGCCAGTAGCAAATGGAACATTG 149
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy     150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy     210 ATTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATGCACA 269
           |||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db      61 ThrSerIleGlyLysAsnMetGlnGlnLeuHisIleLysPheArgAspGlyArgAsnCysThr 80

Qy     270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100

Qy     330 CTCTTCATAGAAGAGAGCAGCGCTTCAGCAATTGCTACCCATGACATCCCTGACTAT 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101 LeuPheIleGluArgSerSerAlaPheSerAlaIleProTyrAspIleProAspTyr 120

Qy     390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy     450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCGTGCAAAAGGGATCAGCCGAT 509
           |||||||||||||||||||||||||||||||||||||:::||||||
Db     141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysArgArgGlySerAlaAsp 160

Qy     510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTTTACCCCACATTGAAT 569
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

Qy     570 GTGACAATGCCTAACAATAAAAATTTCGACAACTATCATCTGGGGGATTCATCACCCG 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ValThrMetProAsnAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy     630 AGCTCAAACCAACAGCACAGCAGAATTGTACATCCAAGAATCAGGAGTAACAGTCTCA 689
           ||||::::||    :::|||||||||||||||||||||||||||||||||||||||||
Db     201 SerThrAsnGlnGlnThrLysLeuTyrIleGlnGluSerGlyValThrValSer 220

Qy     690 ACAAAAAGAAGTCAACAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 ThrLysArgSerGlnGlnThrIleIleIleLeuProAsnIleGlySerArgProValArgGly 240

Qy     750 CAATCAGGCAGGATAAGCATATACTGGACATATTGGTGTCTGAATGTATTCCTAATGATA 809
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GlnSerGlyArgIleSerIleTyrTrpThrTyrTrpIleValLysProGlyAspIleLeuMetIle 260

Qy     810 AACAGTAATGGCAACTTAGTTGCACCTGTTATTAAATTGAAAACAGGGAAAAGC 869
           |||||||||||||||||||||||||||||:::::||||||
Db     261 AsnSerAsnGlyAsnLeuValAlaProValArgPheLysMetArgThrGlyLysLysSer 280

Qy     870 TCTGTAATGAGATCAGGATAAGCATAGACATTGTGTCTCTGAATGTATTACCACCAAAT 929
           |||  :::|||||||||||||||||||||||||||||||||
Db     281 SerValMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrProAsn 300

Qy     930 GGAAGCATCCCACGACAAAACCATTTCAAAATGAACAAAGTTACATATGGAAAATGC 989
           |||||||||||||||||||||||||||||||||||||||||:::|
Db     301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyLysCys 320

Qy     990 CCCAGTATATCAGGCAAAACACTTTAAAGCTGGGATGAGGAATATACCAGAA 1049
           |||||||||||||||||||::::|||||
Db     321 ProLysTyrIleLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGly 340

Qy    1050 AAGCAAATCAGA 1061
```

```
Db     341 LysGlnIleArg 344
           ||||||||||||
```

RESULT 4
AAP70711
ID   AAP70711 standard; protein; 565, AA.
XX
AC   AAP70711;
XX
DT   08-MAR-1991 (first entry)
XX
DE   Equine influenza virus strain H3N8 (EIV-A2) haemagglutinin H3 gene
DE   product.
XX
KW   HA; vaccine; Vaccina.
XX
OS   Equine influenza virus.
XX
FH   Key   Location/Qualifiers
FT   Protein   17..343
FT   /label= HA 1 protein
FT   Protein   345..565
FT   /label= HA 2 protein
XX
PN   WO8607593-A.
XX
PD   31-DEC-1986.
XX
PF   20-JUN-1986;   86WO-US001343.
XX
PR   20-JUN-1985;   85US-00747020.
XX
PA   (BIOT-) BIOTECHN RES PARTNE.
XX
PI   Dale B, Cordell B;
XX
DR   WPI; 1987-007191/01.
DR   N-PSDB; AAN71067.
XX
PT   Preventing equine influenza virus infection - using recombinant vaccines
PT   produced using DNA sequences encoding haemagglutinin and neuraminidase
PT   glyco:proteins.
XX
PS   Disclosure; Fig 2; 63pp; English.
XX
CC   Peptides derived from the haemagglutinin H7 and H3 and neuraminidase N7
CC   and N8 genes may be used to derive antigenic peptides useful in
CC   vaccination against equine influenza virus infection. Abs raised to the
CC   peptides may be used in diagnosis of the infection and construction of
CC   probes to mutated forms of the virus
XX
SQ   Sequence 565 AA;

Alignment Scores:
Pred. No.:   Length: 565
Score: 1.76e-168   Matches: 327
Percent Similarity: 97.97%   Conservative: 10
Best Local Similarity: 95.06%   Mismatches: 7
Query Match: 92.57%   Indels: 0
DB: 1   Gaps: 0

US-10-826-929A-1 (1-1061) x AAP70711 (1-565)

```
Qy      30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGTCTACAGTCAAAACCCAACC 89
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy      90 AGTGGAAACAACACAGCCACCATTATGTCTGGGACACCATGCCAGTAGCAAATGGAACATTG 149
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy     150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

CC particularly horses. The present sequence is a wild type equine influenza
CC virus H3N8 haemagglutinin (HA) protein denoted as PeiwtHA565. This
CC sequence is modified to generate cold-adapted equine influenza virus
XX
SQ Sequence 565 AA;

Alignment Scores:
Pred. No.:   3.46e-170
Score: 1787.00
Percent Similarity: 99.42%
Best Local Similarity: 96.80%
Query Match: 93.46%
DB:

US-10-826-929A-1 (1-1061) x AAY70056 (1-565)

```
Qy     30 ATGAAGACAACAATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCACC 89
          ||||||||||||||||| |||||||||||| |||||||||||||||||||||||||||
Db      1 MetLysThrThrIleIleLeuIleProLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy     90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCAGTAGCAAATGGAACATTG 149
          |||||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db     21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy    150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy    210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAATTGCACA 269
          ||||||||||||||||||| |||||||||||| ::||||||||||||||||||||||
Db     61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy    270 TTAATAGATGCAAATGCTAGGAGACACCCCACTGTGATGTCTTCCAGTATGGAGATTGGGAC 329
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     81 LeuIleAspAlaMetLeuGlyLysAspProHisCysAspValPheGlnHisTyrGluAsnTrpAsp 100

Qy    330 CTCTTCATAGAAAGAAGAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
          |||||||||||||||||||| ||::||||||||| ||||||||||||||||||||||||
Db    101 LeuPheIleGluArgSerAlaPheSerAlaIleAlaThrProTyrTyrAspThrLeuProTyr 120

Qy    390 GGATCGCTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAAATTCCACAGCCAGAGGGATTC 449
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuArgAsnSerSerGlyThrGluGlyPhe 140

Qy    450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
          |||||||||||||||||||||::||||||||||||||||||||| ||||||||||||
Db    141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysArgGlySerAlaAsp 160

Qy    510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
          |||||||||||||||||||||||||||||||::||||||||||||||||||||||
Db    161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180

Qy    570 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGGATTCATCACCCG 629
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy    630 AGCTCCAAACCAACACCAGAGAGAATTGTACATCCAAGAATCAGAGCGAGTAACAGTCTCA 689
          |||||||||::::||||||::|||| |||||||||||||||||||||||||||||
Db    201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220

Qy    690 ACAAAAGAGTCAACAAACAACGATAGTCCCTAATATCGGATCAGACCGTGGGTTAGGGGT 749
          |||||||||||||||::||||||||| ||||||||||||::||||||||||||
Db    221 ThrLysGluSerGlnThrThrIleIleProAsnIleGlySerAspArgProArgValArgGly 240

Qy    750 CAATCAGGCAGGATAAGCATATCTGACCCATTGTAAAACCTGGAGATATCCTAATGATA 809
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    241 GlnSerGlyArgIleSerIleSerTyrThrTrpProThrHisValLysProGlyAspIleLeuMetIle 260

Qy    810 AACAGTAATGGCAACTTAGTTGCTCACCGCGGGGATATTTAAATTGAAAACAGGAAAAGC 869
          |||||||||||||||||||||||||||||||||| |||::||||||||||||||||
Db    261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysIleLysThrGlyLysSer 280

Qy    870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTACACCAAAT 929
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Qy    930 GGAAGCATCCCACGACACAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GlySerIleProAsnAspLysProAsnPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy    990 CCCAAGTATATCAGGCAAAACACTTAAAGCTGGGATGAGAAATATACCAGAA 1049
          ||||||||||||||:::|||||||||||||||||||||||::||||||
Db    321 ProLysTyrIleArgGlnAsnThrLeuLysAlaGlyMetArgAsnValProGlu 340

Qy   1050 AAGCAAATCAGA 1061
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Db    341 LysGlnIleArg 344
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RESULT 3
AAR04943
ID   AAR04943 standard; protein; 565 AA.
XX
AC   AAR04943;
XX
DT   25-MAR-2003 (revised)
DT   02-OCT-1990 (first entry)
XX
DE   Equine hemagglutinin H3 (EIV-A2).
XX
KW   Recombinant vaccines; equine influenza virus; haemagglutinin; H3;
KW   neuraminidase; N8.
XX
OS   Equine influenza virus.
XX
FH   Key   Location/Qualifiers
FT   Region   102..1182
FT   /label= N-terminal HA1 50kD portion
FT   Region   1186..1748
FT   /label= C-terminal HA2 27kD portion
XX
PN   US4920213-A.
XX
PD   24-APR-1990.
XX
PF   21-JUL-1986; 86US-00888250.
XX
PR   20-JUN-1985; 85US-00747020.
XX
PA   (BIOT-) BIOTECH RES PARTNERS LTD.
XX
PI   Dale B, Cordell B;
XX
DR   WPI; 1990-163647/21.
DR   P-PSDB; AAR04943.
XX
PT   Recombinant vaccines against equine influenza virus - produced using DNA
PT   sequences encoding haemagglutinin and neuraminidase glyco-protein(s).
XX
PS   Disclosure; Page ?; 27pp; English.
XX
CC   There are nine neuraminidase (NA) subtypes and twelve haemagglutinin (HA)
CC   subtypes. The strain carrying H3N8 glycoproteins is designated equine
CC   influenza virus (EVI)-A2. The cDNA sequences will be useful in the
CC   construction of diagnostic probes for the disease and of probes for
CC   obtaining new cDNAs of the mutated form of the virus. Recombinant
CC   vaccines are produced. See also AAQ04596-Q04599. (Updated on 25-MAR-2003
CC   to correct PA field.)
XX
SQ   Sequence 565 AA;

Alignment Scores:
Pred. No.:   2.77e-169
Score: 1778.00
Percent Similarity: 98.26%
Best Local Similarity: 95.35%
Query Match: 92.99%

Length: 565
Matches: 328
Conservative: 10
Mismatches: 6
Indels: 0

PT   horses, have a phenotype such as temperature sensitivity or dominant
PT   interference.
XX
PS   Claim 10; Page 93-95; 127pp; English.
XX
CC   The patent discloses experimentally generated cold-adapted equine
CC   influenza viruses, and reassortant influenza A viruses comprising at
CC   least one genome segment of the cold-adapted virus, which confers at
CC   least one identifying phenotype selected from cold-adaptation,
CC   temperature sensitivity, dominant interference and attenuation. These
CC   viruses are used in therapeutic compositions e.g. vaccines for preventing
CC   or treating infections caused by influenza A viruses in animals,
CC   particularly horses. The present sequence is a cold-adapted equine
CC   influenza virus H3N8 haemagglutinin (HA) protein denoted as PeicalHA565.
CC   This sequence is a modified form of the wild type sequence
XX
SQ   Sequence 565 AA;

Alignment Scores:
Pred. No.:
Score: 6.84e-171
Percent Similarity: 1794.00
Best Local Similarity: 99.42%
Query Match: 96.80%
DB: 93.83%
3

Length: 565
Matches: 333
Conservative: 9
Mismatches: 2
Indels: 0
Gaps: 0

US-10-826-929A-1 (1-1061) x AAY70057 (1-565)

Qy   30 ATGAAGACAAACCATTATTTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCACC 89
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Qy   90 AGTGGAAACAACAGCCACCATTATGTCTCGGGACACCACATGCACAAATGGAACATTG 149
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 150 GTAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTACTGAATTAGTTCAGAGC 209
            |||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy 210 ATTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy 270 TTAATAGATGCAATGCTAGGAGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyArgThrProThrValMetSerSerSerMetArgIleGlyThrTrpAsp 100

Qy 330 CTCTTCATAGAAGAAGCAGCGCGCTTCAGCAATGCTACCCATATGACATCCCTGACTAT 389
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 101 LeuPheIleGluGluSerAlaPheSerSerAlaThrProTyrTyrProAspAspTyr 120

Qy 390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy 450 ACATGGACAGGTGTCACTCAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
            ||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db 141 ThrTrpThrGlyValThrGlnAsnGlyArgSerLeuArgSerArgGluSerAlaAsp 160

Qy 510 AGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACCATTGAAT 569
            |||||||||||||||||:|||||||||||||||||||||||||||||||||
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrGluSerGlyAsnSerTyrProThrLeuAsn 180

Qy 570 GTGACAATGCCTAACAATAAAAATTCGACAAACTATACATCTGGGGGATTCATCACCCG 629
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ValThrMetProAsnAsnLysAsnPheAspLysTyrIleLeuTrpGlyIleHisHisPro 200

Qy 630 AGCTCAAACCAACAGCAGACAGATTGTACATCCAAGATCAGGAGTAACAGTGTCA 689
            ||||||:::::||||||||||||||||||||||||||||||||||||
Db 201 SerSerAsnLysGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer 220

Qy 690 ACAAAAGAGTCAACAAAACGATAGTCCCTAATATCGGATCCATGGTTAGGGGT 749
            |||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240
Qy 750 CAATCAGGCAGGATAAGACTATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuThrIle 260
Qy 810 AACAGTAATGGCAACTTAGTTGCACCGCCGGGATATTTAAATTGAAAACAGGGAAAAGC 869
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLysThrGlyLysSer 280
Qy 870 TCTGTAATGAGATCAGATGACCACCATAGACATTGTGTCTCGAATGTATTACCCAAAT 929
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 281 SerValMetArgSerAspAspHisAspArgHisCysValSerGluCysIleThrProAsn 300
Qy 930 GGAAGCATCCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATCATGGAAAATGC 989
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
Qy 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA 1049
            ||||||||||||||||||||||||||||:||||||||||||||||||||||
Db 321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340
Qy 1050 AAGCAAATCAGA 1061
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Db 341 LysGlnIleArg 344

RESULT 2
AAY70056
ID   AAY70056 standard; protein; 565 AA.
XX
AC   AAY70056;
XX
DT   05-JUN-2000 (first entry)
XX
DE   Wild type equine influenza virus H3N8 haemagglutinin protein.
XX
KW   Haemagglutinin protein; wild type HA protein; horse; cold-adaptation;
KW   reassortant virus; temperature sensitivity; dominant interference;
KW   attenuation; antiviral; vaccine; prevention; treatment;
KW   influenza A virus infection.
XX
OS   Equine influenza virus H3N8.
XX
PN   WO200009702-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999;   99WO-US018583.
XX
PR   13-AUG-1998;   98US-00133921.
XX
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Dowling PW, Youngner JS;
XX
DR   WPI; 2000-224339/19.
DR   N-PSDB; AAZ50975.
XX
PT   New cold-adapted equine influenza viruses and reassortant viruses used as
PT   vaccines for treating influenza infections in animals, particularly
PT   horses, have a phenotype such as temperature sensitivity or dominant
PT   interference.
XX
PS   Claim 10; Page 86-88; 127pp; English.
XX
CC   The patent discloses experimentally generated cold-adapted equine
CC   influenza viruses, and reassortant influenza A viruses comprising at
CC   least one genome segment of the cold-adapted virus, which confers at
CC   least one identifying phenotype selected from cold-adaptation. These
CC   temperature sensitivity, dominant interference and attenuation. These
CC   viruses are used in therapeutic compositions e.g. vaccines for preventing
CC   or treating infections caused by influenza A viruses in animals,

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OM nucleic - protein search, using frame_plus_n2p model

Run on:    February 27, 2005, 18:06:24 ; Search time 180 Seconds
                                         (without alignments)
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Searched:       2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:        4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	1794	93.8	565	3	AAY70057	Aay70057 Cold-adap
2	1787	93.5	565	3	AAY70056	Aay70056 Wild type
3	1778	93.0	565	3	AAR04943	Aar04943 Equine he
4	1770	92.6	565	1	AAP70711	Aap70711 Equine in
5	1760	92.1	565	2	AAW44946	Aaw44946 EIV Fonta
6	1527.5	79.9	566	2	AAR63590	Aar63590 Full leng
7	1507.5	78.8	566	5	ABB05767	Abb05767 Full leng
8	1502.5	78.6	566	5	ABB05774	Abb05774 Influenza
9	1493	78.1	329	8	ADR89571	Adr89571 Influenza
10	1475.5	77.2	363	5	ABP53895	Abp53895 Influenza
11	1472	77.0	386	1	AAP40615	Aap40615 Sequence
12	1449.5	75.8	550	5	ABP53894	Abp53894 Influenza
13	1442	75.4	329	5	ABP53897	Abp53897 Influenza
14	1436	75.1	329	5	ABP53896	Abp53896 Influenza
15	1427.5	74.7	566	2	AAW68406	Aaw68406 SIV strai
16	1421	74.3	570	2	AAW01669	Aaw01669 Influenza
17	1421	74.3	570	2	AAW75441	Aaw75441 Influenza
18	1421	74.3	570	4	AAE04951	Aae04951 Influenza
19	1404.5	73.5	570	2	AAW01673	Aaw01673 Influenza
20	1404.5	73.5	571	2	AAW75445	Aaw75445 Influenza
21	1404.5	73.5	571	4	AAE04955	Aae04955 Influenza
22	1398.5	73.1	571	1	AAW01676	Aaw01676 Influenza
23	1398.5	73.1	571	2	AAW75448	Aaw75448 Influenza
24	1398.5	73.1	571	4	AAE04958	Aae04958 Influenza
25	1373	71.8	347	5	AAU76670	Aau76670 Influenza
26	786	41.1	171	8	ADR89583	Adr89583 Influenza
27	664	34.7	146	8	ADR89584	Adr89584 Influenza
28	657	34.4	563	8	ADG43790	Adg43790 Influenza
29	645	33.7	564	5	AAO19499	Aao19499 Recombina
30	641	33.5	570	1	AAP70710	Aap70710 Equine in
31	641	33.5	570	2	AAR04940	Aar04940 Equine he
32	624.5	32.7	571	2	AAW55997	Aaw55997 Protein S
33	624.5	32.7	573	2	ADH29822	Adh29822 Swinepox
34	593	31.0	566	2	AAR08259	Aar08259 Haemagglu
35	593	31.0	566	8	ADL90068	Adl90068 A/PR/8 in
36	588	30.8	566	8	AAW68405	Aaw68405 SIV strai
37	585	30.6	585	8	ADR89585	Adr89585 Influenza
38	580.5	30.4	566	3	AAB29746	Aab29746 Influenza
39	580	30.3	572	2	AAW01670	Aaw01670 Influenza
40	580	30.3	572	2	AAW75442	Aaw75442 Influenza
41	580	30.3	572	4	AAE04952	Aae04952 Influenza
42	538.5	28.2	316	2	ADR90613	Adr90613 Influenza
43	536.5	28.1	412	7	ADJ91998	Adj91998 Influenza
44	528.5	27.6	316	8	ADR90614	Adr90614 Structure
45	521	27.2	562	2	AAR63588	Aar63588 Full leng

ALIGNMENTS

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RESULT 1
AAY70057
ID   AAY70057 standard; protein; 565 AA.
XX
AC   AAY70057;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Cold-adapted equine influenza virus H3N8 haemagglutinin protein.
XX
KW   Haemagglutinin protein; modified HA protein; horse; cold-adaptation;
KW   reassortant virus; temperature sensitivity; dominant interference;
KW   attenuation; antiviral; vaccine; prevention; treatment;
KW   influenza A virus infection.
XX
OS   Equine influenza virus H3N8.
XX
PN   WO20000702-A1.
XX
PD   24-FEB-2000.
XX
PF   12-AUG-1999;    99WO-US018583.
XX
PR   13-AUG-1998;    98US-0013921.
XX
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Dowling PW,  Youngner JS;
XX
DR   WPI; 2000-224339/19..
DR   N-PSDB; AAZ50976.
XX
PT   New cold-adapted equine influenza viruses and reassortant viruses used as
PT   vaccines for treating influenza infections in animals, particularly
```

```
Db       241 ATAGAGTTCTAGATGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCACT  300
                 ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy       301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAGAAGCAGCGCTTTCAGCA    360
             |||||||| || |||||||||||||||||||||||||||||||||||||||||||||
Db       301 GTGANGTCTTTCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCA    360

Qy       361 ATTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG    420
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db       361 GTTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG    420

Qy       421 GAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAA    480
             |||||| |||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       421 GAACATTGGAATTCACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAA    480

Qy       481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA    540
             ||| ||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GTGGATCCTGCAAAAGGGGAATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAG    540

Qy       541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATTTCGACA    600
             ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db       541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATTTCGACA    600

Qy       601 AACTATACATCTCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGAATTGTACA    660
             |||||||||||||||||||| ||||||||||||||| || |||||||||||||||||||
Db       601 AACTATACATCTCTGGGGATTCATCACCCGAGCTCAAACAAAGAGCAGACAAAATTGTACA    660

Qy       661 TCCAAGAATCAGGACGAGCTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTA    720
             ||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
Db       661 TCCAAGAATCAGGACGAGCTAACAGTCTCAACAAAAGAAGTCAACAAACAATAATCCCTA    720

Qy       721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA    780
             | |||||||||||||||||||||||| ||||||||||||| |||||||||||||||||||
Db       721 ACATCGGATCTAGACCGTGGGTCGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA    780

Qy       781 TTGTAAAACCTGGAGATATCCTAATGATAAAACAGTAATGGCAACTTAGTTGCACCGCGGG    840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 TTGTAAAACCTGGAGATATCCTAACGATAAAACAGTAATGGCAACTTAGTTGCACCGCGGG    840

Qy       841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATCGCACCCATAGACA    900
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATCGCACCCATAGACA    900

Qy       901 TTTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCAACGACAAACCATTTCAAA    960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TTTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCACGACAAACCATTTCAAA    960

Qy       961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC   1020
             ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC   1020

Qy      1021 TGGCCACTGGGGATGGAGTTACCAGAAAAGCAAATCAGA   1061
             ||||||||||||||||||||||||||||||||||||||
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Search completed: March 1, 2005, 05:06:21
Job time : 4892 secs

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Db  961  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ATGTGAACAAGTTACATATGAGGAATATCCAGAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy 1021  TGGCCACTGGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
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Db 1021  TGGCCACTGGGATGAGGAATGTACCAGAAAGCAAATCAGA 1061


RESULT 14
AR343239

LOCUS       AR343239                1762 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6579528.
ACCESSION   AR343239
VERSION     AR343239.1  GI:33738757
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1762)
  AUTHORS   Dowling,P.W. and Youngner,J.S.
  TITLE     Cold-adapted equine influenza viruses
  JOURNAL   Patent: US 6579528-A 10 17-JUN-2003;
FEATURES             Location/Qualifiers
     source          1..1762
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match            97.4%;  Score 1033.8;  DB 6;  Length 1762;
Best Local Similarity  98.4%;  Pred. No. 2.3e-235;
Matches 1044;  Conservative  0;  Mismatches 17;  Indels  0;  Gaps  0;

Qy    1  AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGAGACAACCATTATTTGATACTACTGA  60
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGAGACAACCATTATTTGATACTACTGA  60

Qy   61  CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACACACAGCCCACCATTATGTCTGG 120
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACAACCCAACCACCATTATGTCTGG 120

Qy  121  GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy  181  TGACAAATGCTACTGAATTAGTTGTTCGAGCATTTCAATGGGAAAATATGCCAACAACTCAT 240
         || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  TGACAAATGCTACTGAATTAGTTGTTCGAGCATTTCAATGGGAAAATATGCCAACAACTCAT 240

Qy  241  ATAAAGTTCTAGATGGAAGAAATTGCACATTAATGATGCAATGCTAGGAGAGACCCCCACT 300
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  ATAAAGTTCTAGATGGAAGAAATTGCACATTAATGATGCAATGCTAGGAGAGACCCCCACT 300

Qy  301  GTGATGTCTTCCAGTATGGGACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCA 360
         || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  GTGATGTCTTTCAGTATGGGACCTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCA 360

Qy  361  ATTGCTACCCATATGACATCCTGACTATGCATCGCTCCGGTCATTGTAGCATCCTCAG 420
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Db  361  GTTGCTACCCATATGACATCCTGACTATGCATCGCTCCGGTCATTGTAGCATCCTCAG 420

Qy  421  GAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAA 480
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  GAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAA 480

Qy  481  GTGGAGCCTGCAAAGGGGATCAGCCGAGTAGTTCTTTAGCCGACTGGAATTGGCTAACAA 540
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GTGGATCCTGCAAAGGGGATCAGCCGAGTAGTTCTTTAGCCGACTGGAATTGGCTAACAG 540

Qy  541  AATCTGGAAACTCTTACCCCACCATTGACAATGCCTAACATAAAAAAATTTCGACA 600
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  AATCTGGAAACTCTTACCCCACCATTGACAATGCCTAACAATAAAAAAATTTCGACA 600

Qy  601  AACTATACATCTGGGGATTCATCACCCGAGCTCAAACAAACAGAGAATTGTACA 660
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Db  601  AACTATACATCTGGGGATTCATCACCCGAGCTCAAACAAAGAGACAAACGATAGTGTACA 660
         ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||

Qy  661  TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGAGTCAACAAAGATAGTCCCTA 720
         || ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  661  TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGAGTCAACAACAATAATCCCTA 720

Qy  721  ATATCGGATCTAGACCGTGGGTTAGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780
         || ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  721  ACATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCA 780

Qy  781  TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGATGAAACAGTTAGTTGCACCCGCGGG 840
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  TTGTAAAACCTGGAGATATCCTAACGATAAACAGTAATGATGAAACAGTTAGTTGCACCCGCGGG 840

Qy  841  GATATTTTAAATTGAAAACAGGGAAAAGTCTCTGTAATGAGTCGTGTAATGAGATCAGATGCACCCATAGACA 900
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  GATATTTTAAATTGAAAACAGGGAAAAGTCTCTGTAATGAGTCGTGTAATGAGATCAGATGCACCCATAGACA 900

Qy  901  TTTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCAACGACAAACCATTTCAAA 960
         || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  TTTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCAACGACAAACCATTTCAAA 960

Qy  961  ATGTGAACAAGTTACATATGAGGAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  ATGTGAACAAGTTACATATGAGGAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC 1020

Qy 1021  TGGCCACTGGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
         ||||||||||||||||||||| |||||||||||||||||||
Db 1021  TGGCCACTGGGATGAGGAATGTACCAGAAAGCAAATCAGA 1061


RESULT 15
AR455506

LOCUS       AR455506                1762 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 10 from patent US 6685946.
ACCESSION   AR455506
VERSION     AR455506.1  GI:42690326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1762)
  AUTHORS   Dowling,P.W. and Youngner,J.S.
  TITLE     Cold-adapted equine influenza viruses
  JOURNAL   Patent: US 6685946-A 10 03-FEB-2004;
FEATURES             Location/Qualifiers
     source          1..1762
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                     /mol_type="genomic DNA"
ORIGIN

Query Match            97.4%;  Score 1033.8;  DB 6;  Length 1762;
Best Local Similarity  98.4%;  Pred. No. 2.3e-235;
Matches 1044;  Conservative  0;  Mismatches 17;  Indels  0;  Gaps  0;

Qy    1  AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGAGACAACCATTATTTGATACTACTGA  60
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  AGCAAAAGCAGGGGATATTTCTGTCAATCATGAGAGACAACCATTATTTGATACTACTGA  60

Qy   61  CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACACACAGCCCACATTATGTCTGG 120
         || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACAACCCAACCACCATTATGTCTGG 120

Qy  121  GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GACACCATGCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy  181  TGACAAATGCTACTGAATTAGTTCGAGCATTTCAGAGCATTTCAGAGCAAATATGCAACAACTCAT 240
         || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  TGACAAATGCTACTGAATTAGTTCGAGCATTTCAGAGCATTTCAGAGCAAATATGCAACAACTCAT 240

Qy  241  ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGATGCAATGCTAGGAGAGACCCCCACT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGATGCAATGCTAGGAGAGACCCCACT 300
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                                              /mol_type="genomic DNA"

ORIGIN

        Query Match        97.4%;   Score 1033.8; DB 6;  Length 1762;
        Best Local Similarity   98.4%;   Pred. No. 2.3e-235;
        Matches 1044;  Conservative    0;  Mismatches 17;  Indels    0;  Gaps    0;

Qy    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGATGGAAGCAACAACCATTATTTGTGATACTACTGA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGATGGAAGCAACAACCATTATTTTGATACTACTGA 60

Qy   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACACACAGCCACATTATGTCTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGGCCAACACACAGCCACATTATGTCTGG 120

Qy  121 GACACCATGAGTAGCAAATGGAACATTGGACAATTGTAAAACAATAACTGATGACCAAATTGAGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GACACCATGAGTAGCAAATGGAACAATTGGACAATTGTAAAACAATAACTGATGACCAAATTGAGG 180

Qy  181 TGACAAATGCTACTGAATTGTCAGAGCATTCAATAGGGAAAATAATGAACAACTCAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TGACAAATGCTACTGAATTGTCAGAGCATTCAATAGGGAAAATAATGAACAACTCAT 240

Qy  241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
        ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300

Qy  301 GTGATGTCTTTCAGTATGAGAATTGCACCTCTTCATTGTGAGCATCCTCAG 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GTGATGTCTTTCAGTATGAGAATTGGACCTCTTCATTGTGAGCATCCTCAG 360

Qy  361 ATTGCTACCCATATGACATCCCATATGACTATGCATCGTCCGGTCAGTGTAGCATCCTCAG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GTTGCTACCCATATGACATCCCATATGACTATGCATCGTCCGGTCAGTGTAGCATCCTCAG 420

Qy  421 GAACATTAGAATTCACAGCAGAGGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA 480
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Db  421 GAACATTGGAATTCTCTAACAGAGGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA 480

Qy  481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GTGGATCCTGCAAAAGGGAATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAG 540

Qy  541 AATCTGGAAACTCTTACCCACCATGAATGCTAACAATAAAAATTTCGACA 600
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Db  541 AATCTGGAAACTCTTACCCACCATGAATGCTAACAATAAAAATTTCGACA 600

Qy  601 AACTATACATCTGGGGGATTCCTATGATAAACAGCAGAATTAGTTGCAACTTAGTTGTACA 660
        |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  601 AACTATACATCTGGGGGATTCCTATGATAAACAGCAGAATTAGTTGCAACTTAGTTGTACA 660

Qy  661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAAGAAGTCAACAAAAGCGATAGTCCCTA 720
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Db  661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAAGAAGTCAACAAAAGCGATAATCCCTA 720

Qy  721 ATATCGGATCTAGACCGTGGGTTAGGGTTCAGGGGTCAATCAGGATAAGCATATACTGACCA 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ACATCGGATCTAGACCGTGGGTCAGGGGGTCAATCAGGATAAGCATATACTGACCA 780

Qy  781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATAAACAGTGACAACTTGCACCCGCGGG 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TTGTAAAACCTGGAGATATCCTAACGATAAACAGTAATAAACAGTGACAACTTGCACCGCGGG 840

Qy  841 GATATTTTAAATTGAAAACAGGGAAAAGTCTGTAATGAGATCAGATCGACCCCATAGACA 900
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Db  841 GATATTTTAAATTGAAAACAGGGAAAAGTCTGTAATGAGATCAGATCGACCCCATAGACA 900

Qy  901 TTTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAACGACAAAACCATTTCAAA 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 TTTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAACGACAAAACCATTTCAAA 960

Qy  961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACTTTAAAGC 1020
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Qy  241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300
        |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT 300

Qy  301 GTGATGTCTTCCAGTATGAGAATTGCACCTCTTCATTGTGAGCATCCTCAG 360
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Db  301 GTGATGTCTTTCAGTATGAGAATTGGACCTCTTCATTGTGAGCATCCTCAG 360

Qy  361 ATTGCTACCCATATGACATCCCATATGACTATGCATCGTCCGGTCAGTGTAGCATCCTCAG 420
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Db  361 ACATCGGATCTAGACCGTGGGTCAGGGGGTCAATCAGGATAAGCATATACTGACCA 420

Qy  421 GAACATTAGAATTCCTGAGATATCCTAATGAATAACAGTAATAAACAGTTGCACCGCGGG 480
        |||||||| |||||||||||||||||||||  ||||||||||||||||||||||||||||
Db  421 GAACATTGGAATTCCTGAGATATCCTAACGATAAACAGTAATAAACAGTTGCACCGCGGG 480

Qy  481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540
        ||||| |||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  481 GTGGATCCTGCAAAAGGGAATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAG 540

Qy  541 AATCTGGAAACTCTTACCCACCATGAATGCTAACAATAAAAATTTCAAA 600
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AATCTGGAAACTCTTACCCACCATGAATGCTAACAATAAAAATTTCAAA 600

Qy  601 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 660

Qy  721 TGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA 1061
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Db 1021 TGGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA 1061
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RESULT 13
AR254631
LOCUS       AR254631              1762 bp    DNA       linear     PAT 20-DEC-2002
DEFINITION  Sequence 10 from patent US 6482414.
ACCESSION   AR254631
VERSION     AR254631.1  GI:27303652
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1762)
  AUTHORS   Dowling,P.W. and Youngner,J.S.
  TITLE     Cold-adapted equine influenza viruses
  JOURNAL   Patent: US 6482414-A 10 19-NOV-2002;
FEATURES             Location/Qualifiers
     source          1..1762
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RESULT 12

LOCUS   BD244631   1762 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Low temperature-adaptable equine influenza virus.
ACCESSION   BD244631
VERSION   BD244631.1 GI:3054401
KEYWORDS   JP 2002522078-A/7.
SOURCE   Equine influenza virus H3N8
  ORGANISM   Equine influenza virus H3N8
             Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
             Influenzavirus A.
REFERENCE   1 (bases 1 to 1762)
  AUTHORS   Dowling,P.W. and Youngner,J.S.
  TITLE   Low temperature-adaptable equine influenza virus
  JOURNAL   Patent: JP 2002522078-A 7 23-JUL-2002;
             THE UNIVERSITY OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER
             EDUCATION
COMMENT   OS   Equine influenza virus H3N8
             PN   JP 2002522078-A/7
             PD   23-JUL-2002
             PF   12-AUG-1999 JP 2000565137
             PR   13-AUG-1998 US 09/133921
             PI   PATRICIA W DOWLING,JULIUS S YOUNGNER
             PC   C12N15/09,A61K39/145,A61P31/16,C07K14/11,C12N7/04//(C12N7/04,
             PC   C12R1:92),
             PC   C12N15/00
             CC   Low temperature-adaptable equine influenza virus FH Key
             FT   CDS   Location/Qualifiers
             FT   (30)..(1724).

FEATURES   Location/Qualifiers
     source   1..1762
                     /organism="Equine influenza virus H3N8"
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ORIGIN

Query Match   97.4%;   Score 1033.8; DB 6;   Length 1762;
Best Local Similarity 98.4%; Pred. No. 2.3e-235;
Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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        MRNVPEKQIRGIFGAIAGFIENGWEGMVDGWYGFRYQNSEGTGQADLKSTQAAIDQI
        NGKLNRVIERTNEKFHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQH
        TIDLTDAEMNKLFEKTRRQLRENAEDMGGGCFKIYHKCDNACIGSIRNGTYDHYIYRD
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sig_peptide    30..74
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ORIGIN
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Query Match         97.9%;  Score 1038.6;  DB 14;  Length 1762;
Best Local Similarity  98.7%;  Pred. No. 1.7e-236;
Matches 1047;  Conservative  0;  Mismatches  14;  Indels  0;  Gaps  0;

Qy     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA   60

Qy    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGAAAACAACACAGCCACATTATGTCTGG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAACAACACAGCCACATTATGTCTCG  120

Qy   121 GACACCATGCGAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCGAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG  180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT  240

Qy   241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACT  300

Qy   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCA  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCTTTCAGCA  360

Qy   361 ATTGCTACCCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTGCTACCCCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAG  420

Qy   421 GAACATTAGAATTCACAGCAGAGGATTCACATGGACAGTGTCACTCAAAACGGAAGAA  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAACATTGGAATTCACAGCAGAGGATTCACATGGACAGTGTCACTCAAAACGGAAGAGA  480

Qy   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGGATCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA  540

Qy   541 AATCTGGAAACTCTTACCCCACATTGAATGACAATGCTAACAATAAAAATTTCGACA  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AATCTGGAAACTCTTACCCCACATTGAATGACAATGCTAACAATAAAAATTTCGACA  600

Qy   601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACGAATTGTACA  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACGAATTGTACA  660
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Qy   661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAAGAAGTCAACAAACGATAGTCCCTA  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAAGAAGTCAACAAACGATAATCCCTA  720

Qy   721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGGATAAGCAGGATCATATACTGGACCA  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGGATAAGCAGGATCATATACTGGACCA  780

Qy   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAAATGGCAACTTAGTTGCCACCCGGGG  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAAATGGCAACTTAGTTGCCACCCGGGG  840

Qy   841 GATATTTTAAATTGAAAACAGGGAAAAGTCTCGTAATGAATCAGTGATGCCACCCATAGACA  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GATATTTTAAATTGAAAACAGGGAAAAGTCTCGTAATGAATCAGTGATGCCACCCATAGACA  900

Qy   901 TTTGTGTGTCTGAATGTATTATCACCAAATGGAAGCATCCCCAACGACAAACCATTTCAAA  960
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Db   901 TTTGTGTGTCTGAATGTATTATCACCAAATGGAAGCATCCCCAACGACAAACCATTTCAAA  960

Qy   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTTAAAGC  1020

Qy  1021 TGGCCACTGGGATGAGGAATATACCAGAAAGCAAATCAGA  1061
         ||||||||||||||||||||||||||||||||||||||||
Db  1021 TGGCCACTGGGATGAGGAATGTACCAGAAAGCAAATCAGA  1061
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RESULT 11
AF197242
LOCUS       AF197242                1061 bp    mRNA    linear   VRL 08-JAN-2003
DEFINITION  Influenza A virus (A/equine/Florida/1/94 (H3N8)) hemagglutinin
            precursor (HA1) mRNA, partial cds.
ACCESSION   AF197242
VERSION     AF197242.1  GI:6651504
KEYWORDS    .
SOURCE      Influenza A virus (A/equine/Florida/1/94 (H3N8))
  ORGANISM  Influenza A virus (A/equine/Florida/1/94 (H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1061)
  AUTHORS   Lai,A.C., Chambers,T.M., Holland,R.E. Jr., Morley,P.S.,
            Haines,D.M., Townsend,H.G. and Barrandeguy,M.
  TITLE     Diverged evolution of recent equine-2 influenza (H3N8) viruses in
            the Western Hemisphere
  JOURNAL   Arch. Virol. 146 (6), 1063-1074 (2001)
  MEDLINE   21395169
  PUBMED    11504416
REFERENCE   2  (bases 1 to 1061)
  AUTHORS   Lai,A.C.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma
            State University, 306 Life Science East, Stillwater, OK 74078, USA
FEATURES             Location/Qualifiers
     source          1..1061
                     /organism="Influenza A virus
                     (A/equine/Florida/1/94 (H3N8))"
                     /virion
                     /mol_type="mRNA"
                     /isolate="A/equine/Florida/1/94"
                     /db_xref="taxon:217815"
                     /note="H3N8"
     gene            1..1061
                     /gene="HA1"
     CDS             30..>1061
                     /gene="HA1"
                     /codon_start=1
                     /product="hemagglutinin precursor"
                     /protein_id="AAF22346.1"
                     /db_xref="GI:6651505"
                     /translation="MKTIILLLLTHWVYSQNPTSGNNTATLCLGHHAVANGTLVKTI
```

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TITLE        Identification of two antigenically and genetically dinstinct
             lineages of H3N8 equine influenza virus in Sweden
JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 1100)
AUTHORS      Oxburgh,L.H.
TITLE        Direct Submission
JOURNAL      Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology,
             Swedish University of Agricultural Sciences, Biomedical Centre Box
             585, s-751 23 Uppsala, SWEDEN
FEATURES             Location/Qualifiers
     source          1..1100
                     /organism="Influenza A virus (A/equi 2/Soderala/94 (H3N8))"
                     /virion
                     /mol_type="genomic RNA"
                     /serotype="H3N8"
                     /isolate="A/equi 2/Soderala/94"
                     /db_xref="taxon:217821"
     mRNA            <30..>1100
     CDS             30..>1100
                     /codon_start=1
                     /product="hemagglutinin HA1 subunit"
                     /protein_id="CAA74386.1"
                     /db_xref="GI:2765370"
                     /db_xref="GOA:O56856"
                     /db_xref="UniProt/TrEMBL:O56856"
                     /translation="MKTIILILLLIHCVYSQNPISGNNTATLCLGHHAVANGTLVKTI
                     TDDQIEVTNATELVQSISIGKICNNSYRVLDGRNCTLIDAMLGDPHCDVFQYENWDLF
                     IERSAFSNCYPYDIPDYASLRSIVASLGTLEFTAEGFTWTGVTQNGRSGACKRGSAD
                     SFFSRLNWLTKSGNSYPTLNVTMPNNKNFDKLYIWGIHHPSSNQQQTELYIQESGRVT
                     VSTKRSQQTVIPNIGSRPWVRGQSGRISIYWTIVKPGDILMINSNGNLVAPRGYFKLK
                     TGKSSVMRSDAPIDICVSECITPNGSIPNDKPFQNVNKVTYGKCPKYIRQNTLKLATG
                     MRNVPEKQIRGIFGAIAGFIENG"
     exon            30..1100
                     /number=1
     sig_peptide     30..75
ORIGIN

Query Match             97.9%;  Score 1039.2;  DB 14;  Length 1100;
Best Local Similarity   98.8%;  Pred. No. 1.3e-236;
Matches 1047;  Conservative    0;  Mismatches  13;  Indels   0;  Gaps    0;

Qy          2 GCAAAAGCAGGGAGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGAC   61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCAAAAGCAGGGAGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGAT   61

Qy         62 CCATTGGGTCTACAGTCAAAACCCAACCAGTGGAAACAACACAGCCCACATTATGTCTGGG  121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCATTGTGTCTACAGTCAAAACCCAATCAGTGGCAACAACACAGCCCACATTATGTCTGGG  121

Qy        122 ACACCATGCAGTAGCAACATTGGTAAAACATTGGTAAAAACAATAACTACTGATGACCAAATTGAGGT  181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACACCATGCAGTAGCAACATTGGTAAAATACTGGTAAAAACAATAACTACTGATGACCAAATTGAGGT  181

Qy        182 GACAAATGCTACTACTGAATTAGTTCAGAGCATTCAATAGGGAAAAATATGCCAACAACTCATA  241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GACAAATGCTACTACTGAATTAGTTCAGAGCATTCAATAGGGAAAAATATGCAACAACTCATA  241

Qy        242 TAAAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACTG  301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TAGAGTTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACTG  301

Qy        302 TGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCCGCTTTCAGCAA  361
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TGATGTCTTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCAA  361

Qy        362 TTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTTGTAGCCATCCTCAGG  421
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGCTACCCATATGACATCCCTGACTATGCATCGCTCCGGTTGTAGCCATCCTTAGG  421

Qy        422 AACATTAGAATTCACAGCAGGAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAAG  481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AACATTGAATTCACAGCAGGAGGGATTCACATGGACAGGTGTCACTCAAAAACGGAAGAAG  481
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Qy        482 TGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA  541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA  541

Qy        542 ATCTGAAACTCTTACCCCACATTGAAATGTGACAATGCCTAACAATAAAATTCGACAA  601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 ATCTGAAACTCTTACCCCACATTGAAATGTGACAATGCCTAACAATAAAAATTCGACAA  601

Qy        602 ACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACACAGCAGACAGAATTGTACAT  661
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACACAGCAGACAGAATTGTACAT  661

Qy        662 CCAAGAATCAGGACGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAGTAGTCCCTAA  721
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCAAGAATCAGGACGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAGTAATCCCTAA  721

Qy        722 TATCGGATCTAGACCGTGGTTAGGGGTCAATCAGGCAGGATAAGCAGCATATACTGGACCAT  781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 TATCGGATCTAGACCGTGGGTCAGGGGTCAATCAGGCAGGATAAGCAGCATATACTGGACCAT  781

Qy        782 TGTAAAACCTGGAGATATCCTAATGATAAAACGATAATGGCAACTTAGTTGCACCCGGGG  841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 TGTAAAACCTGGAGATATCCTAATGATAAACGATAATGGCAACTTAGTTGCACCGCGGGG  841

Qy        842 ATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAATGCAGATCAGATGCACCCATAGACAT  901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 ATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAATGCAGATCAGATGCACCCATAGACAT  901

Qy        902 TTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAACGACAAAACCATTTCAAAA  961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 TTGTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAACGACAAAACCATTTCAAAA  961

Qy        962 TGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGCT  1021
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGCT  1021

Qy       1022 GGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCAGA  1061
              ||||||||||||||||||||||||||||||||||||||||
Db       1022 GGCCACTGGGATGAGGAATGTACCAGAAAAGCAAATCAGA  1061
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RESULT 10
FLAHAH3F
LOCUS       FLAHAH3F      1762 bp  ss-RNA      linear      VRL 29-NOV-1996
DEFINITION  Influenza A/Equine/Kentucky/1/91 hemagglutinin (HA1) gene, complete
            cds.
ACCESSION   L39918
VERSION     L39918.1    GI:722411
KEYWORDS    .
SOURCE      Influenza A virus (strain A/equine/Kentucky/1/91)
  ORGANISM  Influenza A virus (strain A/equine/Kentucky/1/91)
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1762)
AUTHORS     Daly,J.M., Lai,A.C., Binns,M.M., Chambers,T.M., Barrandeguy,M. and
            Mumford,J.A.
TITLE       Antigenic and genetic evolution of equine H3N8 influenza A viruses
JOURNAL     J. Gen. Virol. 77 (Pt 4), 661-671 (1996)
MEDLINE     96203953
PUBMED      8627254
FEATURES             Location/Qualifiers
     source          1..1762
                     /organism="Influenza A virus (strain
                     A/equine/Kentucky/1/91)"
                     /mol_type="genomic RNA"
                     /strain="Equine-2"
                     /isolate="A/Equine/Kentucky/1/91"
                     /db_xref="taxon:38828"
                     /clone="2554"
     gene            30..1727
                     /gene="HA1"
     CDS             30..1727
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DEFINITION   Influenza A/Equine/Florida/1/93 hemagglutinin (HA1) gene, complete
              cds.
ACCESSION   L39916
VERSION   L39916.1 GI:722407
KEYWORDS   .
SOURCE   Influenza A virus (strain A/equine/Florida/1/93)
  ORGANISM   Influenza A virus (strain A/equine/Florida/1/93)
              Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
              Influenzavirus A.
REFERENCE   1 (bases 1 to 1762)
  AUTHORS   Daly,J.M., Lai,A.C., Binns,M.M., Chambers,T.M., Barrandeguy,M. and
              Mumford,J.A.
  TITLE   Antigenic and genetic evolution of equine H3N8 influenza A viruses
  JOURNAL   J. Gen. Virol. 77 (Pt 4), 661-671 (1996)
  MEDLINE   96203953
  PUBMED   8627254
FEATURES   Location/Qualifiers
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                     /clone="2763"
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                     /protein_id="AAB36978.1"
                     /db_xref="GI:722408"
                     /translation="MKTIILLLLTHWVYSQNPTSGNNTATLCLGHHAVANGTLVKTI
                     TDDQIEVTNATELVQSISIGKICNNSYRVLDGRNCTLIDAMLGDPHCDVFQYENWDLF
                     IERSSAFSNCYPYDIPDYASLRSIVASSGTLEFTAEGFTWTGVTQNGRSGACKRGSAD
                     SFFSRLNWLTKSGNSYPTLNVTMPNNKNFDKLYIWGIHHPSSNQEQTKLYIQESGRVT
                     VSTKRSQQTIIPNIGSRPWVRGQSGRISIYWTIVKPGDILMINSNGNLVAPRGYFKLK
                     TGKSSVMRSDAPIDICVSECITPNGSISNDKPFQNVNKVTYGKSCPKYIRQNTLKLATG
                     MRNVPEKQIRGIFGAIAGFIENGWEGMVDGWYGFRYQNSEGTGQAADLKSTQAAIDQI
                     NGKLNRVIERTNEKFHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQH
                     TIDLTDAEMNKLFEKTRRQLRENAEDMGGGCFKIYHKCDNACIGSIRNGTYDHYIYRD
                     EALNRRFQIKGVELKSGYKDWILWISFTISCFLICVVLLGFIMWACQKGNIRCNICI"
     sig_peptide   30..74
                     /gene="HA1"
                     /note="putative"
     mat_peptide   75..1724
                     /gene="HA1"
                     /product="hemagglutinin"
                     /note="includes HA1 and HA2"
     mat_peptide   75..1061
                     /gene="HA1"
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ORIGIN

Query Match   98.2%; Score 1041.8; DB 14; Length 1762;
Best Local Similarity   98.9%; Pred. No. 2.9e-237;
Matches 1049; Conservative   0; Mismatches 12; Indels   0; Gaps   0;

Qy   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTTGATACTACTGA 60

Qy   61 CCCATTGGGTCTCACAGTCAAAACCCAACCAGTCGAAACAACACAGCCACCATTATGTCTGG 120
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   61 CCCATTGGGTCTCACAGTCAAAACCCAACCAGTCGAACACAACACAGCCACCATTATGTCTGG 120

Qy   121 GACACCATGCAGTAGCAAATGGAACATTGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCAGTAGCAAATGGAACATTGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGG 180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
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Db   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT 240
Qy   241 ATAGAGTTCTAGATGGGAAGAAATTGCACATTAATAGATGATGCATTAGATGGGAAAAATTGCACATTAATAGATGATGCATTAG 300
Db   241 ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
           ATAGAGTTCTAGATGGGAAGAAATTGCACATTAATAGATGATGCATTAGATGGGAAAAATTGCACATTAATAGATGATGCATTAG 300
Qy   301 GTGATGTCTTCAGTATGGGAATTGGGACCTCTTCATAGAAAGAGCAGCGCGCTTTCAGCA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTGATGTCTTCAGTATGGGAATTGGGACCTCTTCATAGAAAGAGCAGCGCGCTTTCAGCA 360
Qy   361 ATTGCTACCCATATGACATCCCGACTATGCATGCTCCGGTCCATTGTAGCATCCTCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATTGCTACCCATATGACATCCCGACTATGCATGCTCCGGTCCATTGTAGCATCCTCAG 420
Qy   421 GAACATTAGAATTCACAGCAGAGGGATTCACATGACAGAGTGTCACTCAAAACGGAAGAA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAACATTGGAATTCACAGCAGAGGGATTCACATGACAGAGTGTCACTCAAAACGGAAGAA 480
Qy   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA 540
Qy   541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAAATGCCTAACAATAAAATTTCGACA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AATCTGGAAACTCTTACCCCACATTGAATGTGACAAATGCCTAACAATAAAATTTCGACA 600
Qy   601 AACTATACATCTGGGGAGTCATCACCCGAGCTCAAACCAACAGCAGAGAATTGTACA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACTATACATCTGGGGAGTCATCACCCGAGCTCAAACCAAGAGCAGAGACAAAATTGTACA 660
Qy   661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTA 720
           ||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Db   661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACAATAATCCCTA 720
Qy   721 ATATCGGATCTAGACCGTGGTTAGGGTCAATCAGGGATATAAGCATCAGGGACCATACTGGACCA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACATCGGATCTAGACCGTGGTTAGGGTCAGGGTCAATCAGGGATATAAGCATCAGGGACCATACTGGACCA 780
Qy   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGG 840
Qy   841 GATATTTTAAATTGAAAACAGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACA 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GATATTTTAAATTGAAAACAGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACA 900
Qy   901 TTTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCCAACGACAAAACCATTTCAAA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCAACGACAAAACCATTTCAAA 960
Qy   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
Qy   1021 TGGCCACTGGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
           ||||||||||||||||||||||||||||||||||||||||
Db   1021 TGGCCACTGGGATGAGGAATGTACCAGAAAGCAAATCAGA 1061

RESULT 9
EIVY14058
LOCUS   EIVY14058   1100 bp   RNA   linear   VRL 11-JAN-2003
DEFINITION Influenza A virus (A/equi 2/Soderala/94 (H3N8)) gene for
            hemagglutinin HA1 subunit, isolate A/equi 2/Soderala/94.
ACCESSION   Y14058
VERSION   Y14058.1 GI:2765369
KEYWORDS   hemagglutinin HA1 subunit.
SOURCE   Influenza A virus (A/equi 2/Soderala/94 (H3N8))
  ORGANISM Influenza A virus (A/equi 2/Soderala/94 (H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1 (bases 1 to 1100)
  AUTHORS   Oxburgh,L., Akerblom,L., Fridberger,T., Klingeborn,B. and Linne,T.

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Db  841 AAAATGAAACAGGGAAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACATTGTGCG 900

Qy   69 GTCTACAGTCAAAACCCAGCAGTGGAAACAACACAGCGACCACACATATGTCTGGGACACCAT 128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTCTACAGTCAAAACCCAGCAGTGGAAACAACACAGCGACCACACATATGTCTGGGACACCAT 120

Qy  909 TCTGAATGTATTACACCAAATGGAAGCAGGAGCATCCCCAGCATATCAGGCAAAACACTTCAAAATGTGAAC 968
Qy  129 GCAGTAGCAAATGGAACAGTTGGTAAAAAACAACAATAACTGATGACGAGGTGACAAAT 188
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GCAGTAGCAAATGGAACAGTTGGTAAAAACAATAACTGATGACGAGGTGACAAAT 180

Db  901 TCTGAATGTATTACACCAAATGGAAGCAGGAGCATCCCCAGCATATCAGGCAAAACACTTCAAAATGTGAAC 960

Qy  189 GCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTT 248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCATATAGAGTT 240

Qy  249 CTAGATGGAAGAAATTGCACATTAATAGATGCAATTGCAATGCTAGGAGACACCCCACTGTGATGTC 308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CTAGATGGAAGAAATTGCACATTAATAGATGCAATTGCAATGCTAGGAGACACCCCACTGTGATGTC 300

Qy  309 TTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCGCGCTTTCAGCAATTGCTAC 368
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 TTCCAGTATGAGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCGCTTTCAGCAATTGCTAC 360

Qy  369 CCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTA 428
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CCATATGACATCCCTGACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTG 420

Qy  429 GAATTCACAGCAGCAGGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCC 488
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GAATTCACAGCAGCAGGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCC 480

Qy  489 TGCAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGA 548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TGCAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGA 540

Qy  549 AACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATTCGACAAACTATAC 608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AACTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATTCGACAAACTATAC 600

Qy  609 ATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAA 668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 ATCTGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAA 660

Qy  669 TCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAACGATAGTCCCTAATATCGGA 728
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 TCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAACGATAATCCCTAATATCGGA 720

Qy  729 TCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAA 788
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAA 780

Qy  789 CCTGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTT 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CCTGAGATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTT 840

Qy  849 AAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTG 908
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 AAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGCG 900

Qy  909 TCTGAATGTATTACACCAAATGGAAGCATCCCCACGACAAACCATTTCAAAATGTGAAC 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 TCTGAATGTATTACACCAAATGGAAGCATCCCCACGACAAACCATTTCAAAATGTGAAC 960

Qy 1029 GGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
          ||||||||||||||||||||||||||||||||
Db 1021 GGGATGAGGAATATACCAGAAAGCAAATCAGA 1053
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Qy  969 AAAGTTACATATGGAAAATGCCCAAGTAATATCAGGGATATATCAGGCAAAACACTTCGGCCACT 1028
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 AAAGTTACATATGGAAAATGCCCAAGTAATATCAGGGATATATCAGGCAAAACACTTCGGCCACT 1020
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Qy 1029 GGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
          ||||||||||||||||||||||||||||||||
Db 1021 GGGATGAGGAATATACCAGAAAGCAAATCAGA 1053
```

RESULT 7
EIVY14060
LOCUS   EIVY14060   1060 bp   RNA   linear   VRL 11-JAN-2003
DEFINITION Influenza A virus (A/equi 2/Bollnas/96 (H3N8)) gene for
            hemagglutinin HA1 subunit, isolate A/equi 2/Bollnas/96.
ACCESSION   Y14060
VERSION   Y14060.1 GI:2765373
KEYWORDS   hemagglutinin HA1 subunit.
SOURCE   Influenza A virus (A/equi 2/Bollnas/96 (H3N8))
  ORGANISM Influenza A virus (A/equi 2/Bollnas/96 (H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1 (bases 1 to 1060)
  AUTHORS   Oxburgh,L., Akerblom,L., Fridberger,T., Klingeborn,B. and Linne,T.
  TITLE   Identification of two antigenically and genetically dinstinct
            lineages of H3N8 equine influenza virus in Sweden
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1060)
  AUTHORS   Oxburgh,L.H.
  TITLE   Direct Submission
  JOURNAL   Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology,
            Swedish University of Agricultural Sciences, Biomedical Centre Box
            585, S-751 23 Uppsala, SWEDEN
FEATURES   Location/Qualifiers
     source   1..1060
                     /organism="Influenza A virus (A/equi 2/Bollnas/96 (H3N8))"
                     /virion
                     /mol_type="genomic RNA"
                     /serotype="H3N8"
                     /isolate="A/equi 2/Bollnas/96"
                     /db_xref="taxon:217819"
     mRNA   <22..1060
     CDS   22..>1060
                     /codon_start=1
                     /product="hemagglutinin HA1 subunit"
                     /protein_id="CAA74388.1"
                     /db_xref="GI:2765374"
                     /db_xref="GOA:O56858"
                     /db_xref="UniProt/TrEMBL:O56858"
                     /translation="MKTTIILLILTHWVYSQNPTSGNNTATLCLGHHAVANGTLVKTI
                     TNDQIEVTNATELVQSISIGKICNNSYRVLDGRNCTLIDAMLGDPHCDVFQYENWDLF
                     IERSSAFSNCYPYDIPDYASLRSIVASSGTLEFTAEGFTWTGVTQNGRSGACKRGSAD
                     SFFSRLNWLTKSGNSYPTLNVTMPNNKNFDKLYIWGIHHPSSNQQTELYIQESGRVT
                     VSTKRSQQTIIFNIGSRPWVRGQSGRISIYWTIVKPGDILMINSNGNLVAPRGYFKLK
                     TGKSSVMRSDAPIDICASECITPNGSITPNGSIFNDKFPQNVNKVTYGKCPKYIRQNTLKLATG
                     MRNVPEKQIRGI"
ORIGIN

Query Match   98.2%; Score 1041.8; DB 14; Length 1060;
Best Local Similarity - 99.3%; Pred. No. 3.1e-237;
Matches 1046; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

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Qy    9 CAGGGGATATTTCTGTCAATCATGAAGACAACCATTATTTGATACTACTGACCCATTGG 68
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CAGGGGATATTTCTGTCAATCATGAAAACAACCATTATTTGATACTACTGACCCATTGG 60
```

RESULT 8
FLAHAH3D
LOCUS   FLAHAH3D   1762 bp ss-RNA   linear   VRL 29-NOV-1996

```
TNDQIEVTNATELVQSISIGKICNNSYRVLDGRNCTLIDAMLGDPHCDVFQYENWDLF
IERSSAFSNCYPYDIPDYASLRSIVASSGTLEFTAEGFTWTGVTQNGRSGACKRGSAD
SFFSRLNWLTKSGNSYPTLNVTMPNNKNFDKLYIWGIHKPSSNQQOTELYIQESGRVT
VSTKRSQQTIIPNGSRPWVRGQSGRISIYWTIVKPGDILMINSNGNLVAPRGYFKLK
TGKSSVMRSDAPIDICASECITPNGSIPNDKPFQNVNKVTYGKCPKYIRQNTLKLATG
MRNVPEKQIRGI"
22. .1060
/number=1
22. .67
```

ORIGIN

exon

sig_peptide

```
Query Match          98.3%;  Score 1043.4;  DB 14;  Length 1060
Best Local Similarity 99.4%;  Pred. No. 1.3e-237;
Matches 1047;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;
```

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Qy        9 CAGGGGATATTTCTGTCAATCATGAGACAACACCATTATTTGATACTACTGACCCATTGG   68
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 CAGGGGATATTTCTGTCAATCATGAGACAACACCATTATTTGATACTACTGACCCATTGG   60

Qy       69 GTCTACAGTCAAAACCCACCAGTGAAACAACACAGCCACATTATGTCTGGACACCAT    128
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       61 GTCTACAGTCAAAACCCACCAGTGAAACAACACAGCCCACATTATGTCTGGACACCAT    120

Qy      129 GCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGGTGACAAAT    188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCAGTAGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGGTGACAAAT    180

Qy      189 GCTACTGAATTAGTTCAGAGCATTCAATAGGGAAAAATATGCAACAACTCATATAAAGTT    248
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GCTACTGAATTAGTTCAGAGCATTCAATAGGGAAAAATATGCAACAACTCATATAGAGTT    240

Qy      249 CTAGATGGAGAAATTGCACATTAATAGATGCAATGCTAGGAGACACCCCACTGTGATGTC    308
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CTAGATGGAGAAATTGCACATTAATAGATGCAATGCTAGGAGACACCCCACTGTGATGTC    300

Qy      309 TTCCAGTATGACATCCCTGACTATGCATCCGTCCGGTCCATTGTAGCATCCTCAGGAACATTA    368
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 TTCCAGTATGACATCCCTGACTATGCATCCGTCCGGTCCATTGTAGCATCCTCAGGAACATTA    360

Qy      369 CCATATGACATCCCTGACTATGCGCTCCGGTCCATTGTAGCATCGTCCTCAGGACATTG    428
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CCATATGACATCCCTGACTATGCGCTCCGGTCCATTGTAGCATCGTCCTCAGGACATTG    420

Qy      429 GAATTCACAGCAGCAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCC    488
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GAATTCACAGCAGCAGGGATTCACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCC    480

Qy      489 TGCAAAAGGGGATCCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGA    548
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TGCAAAAGGGGATCCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGA    540

Qy      549 AACTCTTACCCCACATTGAANTGTGACAATGCCTAACAATAAAAATTTGACAAACTATAC    608
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 AACTCTTACCCCACATTGAANTGTGACAATGCCTAACAATAAAAATTTGACAAACTATAC    600

Qy      609 ATCTGGGGATTCATCACCCGAGTCCAAACCAACAGCAGACAGAATTGTACATCCAAGAA    668
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 ATCTGGGGATTCATCACCCGAGTCCAAACCAACAGCAGACAGAATTGTACATCCAAGAA    660

Qy      669 TCAGGACGAGTAACAAGTCTCAACAAAAGAAGTCAACAACGATAGTCCCTAATATCGGA    728
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TCAGGACGAGTAACAAGTCTCAACAAAAGAAGTCAACAACGATAATCCCTAATATCGGA    720

Qy      729 TCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATAACTACTGGACCATTGTAAAA    788
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATAACTACTGGACCATTGTAAAA    780

Qy      789 CCTGAGATATCCTAATGAAAACAGTAAACAGTAATGCAACTTAGTTGCACCGCGGGGATATTTT    848
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCTGGAGATATCCTAATGAAAACAGTAATAAACAGTAATGCAACTTAGTTGCACCGCGGGGATATTTT    840

Qy      849 AAATTGAAAACAGGAAAAGTCTCTGTAATGAATGATCAAGATCGACCACCATAGACATTGTGTG    908
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACCAACAGCAGACAGAATTGTACA    660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AACTATACATCTGGGGATTCATCACCCGAGCTCAAACCAACCAACAGCAGACAGAATTGTACA    660

Qy      661 TCCAAGAATCAGGACGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACCGATAGTCCCTA    720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TCCAAGAATCAGGACGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACCGATAGTCCCTA    720

Qy      721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATAACTACTGGACCA    780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATAACTACTGGACCA    780

Qy      781 TTGTAAAAACCTGGAGATATCCTAATGATAAAACAGTAATAAACAGTAATGCAACTTAGTTGCACCGCGGG    840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TTGTAAAAACCTGGAGATATCCTAATGATAAAACAGTAATAAACAGTAATGCAACTTAGTTGCACCGCGGG    840

Qy      841 GATATTTTAAATTGAAAACAGGGAAAAGTCTCTGTAATGAATGATCAGATGCACCCATAGACA    900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GATATTTTAAATTGAAAACAGGGAAAAGTCTCTGTAATGAATGATCAGATGCACCCATAGACA    900

Qy      901 TTTGTGTGTCTGAATGTATTACACCCAAATGGAAGCATCCCAACGACAAACCATTTCAAA    960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TTTGTGTGTCTGAATGTATTACACCCAAATGGAAGCATCCCAACGACAAACCATTTCAAA    960

Qy      961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC    1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATCAGGCAAAACACTTTAAAGC    1020

Qy     1021 TGGCCACTGGATGAGGAATATACCAGAAAAGCAAATCAGA    1061
            ||||||||||||||||||||||||||||||||||||||||
Db     1021 TGGCCACTGGATGAGGAATGTACCAGAAAAGCAAATCAGA    1061
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RESULT 6
EIVY14059

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LOCUS       EIVY14059               1060 bp    RNA     linear   VRL 11-JAN-2003
DEFINITION  Influenza A virus (A/equi 2/Alvdalen/96(H3N8)) gene for
            hemagglutinin HA1 subunit, isolate A/equi 2/Alvdalen/96.
ACCESSION   Y14059
VERSION     Y14059.1  GI:2765371
KEYWORDS    hemagglutinin HA1 subunit.
SOURCE      Influenza A virus (A/equi 2/Alvdalen/96(H3N8))
ORGANISM    Influenza A virus (A/equi 2/Alvdalen/96(H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1060)
AUTHORS     Oxburgh,L., Akerblom,L., Fridberger,T., Klingeborn,B. and Linne,T.
TITLE       Identification of two antigenically and genetically distinct
            lineages of H3N8 equine influenza virus in Sweden
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 1060)
AUTHORS     Oxburgh,L.H.
TITLE       Direct Submission
JOURNAL     Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology,
            Swedish University of Agricultural Sciences, Biomedical Centre Box
            585, S-751 23 Uppsala, SWEDEN
FEATURES             Location/Qualifiers
     source          1..1060
                     /organism="Influenza A virus (A/equi 2/Alvdalen/96 (H3N8))"
                     /virion
                     /mol_type="genomic RNA"
                     /serotype="H3N8"
                     /isolate="A/equi 2/Alvdalen/96"
                     /db_xref="taxon:217820"
     mRNA            <22..>1060
     CDS             22..>1060
                     /codon_start=1
                     /product="hemagglutinin HA1 subunit"
                     /protein_id="CAA74387.1"
                     /db_xref="GI:2765372"
                     /db_xref="GOA:O56857"
                     /db_xref="UniProt/TrEMBL:O56857"
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CDS            /gene="HA1"
               30..1727
               /gene="HA1"
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               /protein_id="AAB36976.1"
               /db_xref="GI:722404"
               /translation="MKTTIILLLLTHWYSQNPTSGNNTATLCLGHHAVANGTLVKTI
               TDDQIEVTNATELVQSISIGKICNNSYRVLDGRNCTLIDAMLGDPHCDVFQYENWDLF
               IERSSAFSNCYPYDIPDYASLRSIVASSGTLEFTAEGFTWTGVTQNGRSGACKRGSAD
               SFFSRLNWLTKSGNSYPTLNVTMPNNKNFDKLYIWGIHHPSSNQQOTELYIQESGRVT
               VSTKRSQQTIIPNIGSRPWVRGQSGRISIYWTIVKPGDILMINSNGNLVAPRGYFKLK
               TGKSSVMRSDAPIDICVSECITPNGSIPNDKPFQNVNKVTYGKCPKYIRQNTLKLATG
               MRNVPEKQIRGIPGAIAGFIENGWEGMVDGWYGFRYQNSEGTQAADLKSTQAAIDQI
               NGKLNRVIERTNEKPHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQH
               TIDLTDAEMNKLFEKTRRQLRENAEDMGGGCFKIYHKCDNACIGSIRNGTYDHYIYRD
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sig_peptide    30..74
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               /note="putative"
mat_peptide    75..1724
               /gene="HA1"
               /product="hemagglutinin"
               /note="includes HA1 and HA2"
mat_peptide    75..1061
               /gene="HA1"
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ORIGIN

Query Match          98.8%;  Score 1048.2;  DB 14;  Length 1762;
Best Local Similarity 99.2%;  Pred. No. 8.6e-239;
Matches 1053;  Conservative 0;  Mismatches 8;  Indels 0;  Gaps 0;

Qy     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACAACCATTATTTTGATACTACTGA   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGCAAAAGCAGGGGATATTTCTGTCAATCATGAAGACAACAACCATTATTTTGATACTACTGA   60

Qy    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAAAACACACAGCCACATTATGTCTGG  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCCATTGGGTCTACAGTCAAAACCCAACCAGTGCAAAACACACAGCCACATTATGTCTGG  120

Qy   121 GACACCATGCAGTAGCAAATGGTAAAAACAATAACTGATGACCAAATTGAGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GACACCATGCAGTAGCAAATGGTAAAAACAATAACTGATGACCAAATTGAGG  180

Qy   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT  240
         ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   181 TGACAAATGCTACTGAATTAGTTCAGAGCATTTCAATAGGGAAAATATGCAACAACTCAT  240

Qy   241 ATAAAGTTCTAGATGAAGAAATTGCACATTAATAGATGCATGGAGGAGACCCCCCACT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATAGAGTTCTAGATGAAGAAATTGCACATTAATAGATGCATGGAGGAGACCCCCCACT  300

Qy   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTTCATAGAAGAAGCAGCGCTTTCAGCA  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTGATGTCTTCCAGTATGAGAATTGGGACCTTCATAGAAGAAGCAGCGCTTTCAGCA  360

Qy   361 ATTGCTACCCATATGACATCCCTGACTATCGCTCCGGTCTCCATTGTAGCATCCTCAG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATTGCTACCCATATGACATCCCTGACTATCGCTCCGGTCTCCATTGTAGCATCCTCAG  420

Qy   421 GAACATTAGCCATTCACAGCAGAGGGATTCACATGACATCCCTGACTGTCACTGCTAACAA  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAACATTAGCCATTCACAGCAGAGGGATTCACATGACATCCCTGACTGTCACTGCTAACAA  480

Qy   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACAA  540

Qy   541 AATCTGGAAACTCTTACCCCACATTGAAATGCTAACAATAAAAATTCGACA  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AATCTGGAAACTCTTACCCCACATTGAAATGCTAACAATAAAAATTCGACA  600
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Db   421 GAACATTAGCCATTCACAGCAGAGGGATTCACATGACATCCCTGACTGTCACTGCTAACAA  480
Qy   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACACA  540
Db   481 GTGGAGCCTGCAAAAGGGGATCAGCCGATAGTTTCTTTAGCCGACTGAATTGGCTAACACA  540
Qy   541 AATCTGGAAACTCTTACCCCACATTGAAATGCTAACAATAAAAATTCGACA  600
Db   541 AATCTGGAAACTCTTACCCCACATTGAAATGCTAACAATAAAAATTCGACA  600
Qy   601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACACGCAGAATTGTACA  660
Db   601 AACTATACATCTGGGGGATTCATCACCCGAGCTCAAAACCAACACGCAGAATTGTACA  660
Qy   661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTA  720
Db   661 TCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAATCCCTA  720
Qy   721 ATATCGGATCTAGACCGTGGGTTAGGGGTCCAATCAGCGGCAGGATAAGCATATACTGGACCA  780
Db   721 ATATCGGATCTAGACCGTGGGTTAGGGGTCAGGGTCAATCAGGCAGGATAAGCATATACTGGACCA  780
Qy   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGCGAACTTAGTTGCACCGCGGG  840
Db   781 TTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGCGAACTTAGTTGCACCGCGGG  840
Qy   841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAACAAGTCTGTAATGAGATCAGATAGACA  900
Db   841 GATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAACAAGTCTGTAATGAGATCAGATAGACA  900
Qy   901 TTTGTGTCTGAATGTATTACACCACGTAATTACACCAAGAAGCATCCCCAACCATTTCAA  960
Db   901 TTTGTGTCTGAATGTATTACACCACGTAATTACACCAAGAAGCATCCCCAACCATTTCAA  960
Qy   961 ATGTGAACAAGTTACATATGGAAAATGCCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
Db   961 ATGTGAACAAGTTACATATGGAAAATGCCCCCAAGTATATCAGGCAAAACACTTTAAAGC 1020
Qy  1021 TGGCCACTGGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
Db  1021 TGGCCACTGGGATGAGGAATATACCAGAAAGCAAATCAGA 1061
```

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RESULT 5
FLAHAH3B
LOCUS       FLAHAH3B      1762 bp ss-RNA     linear     VRL 29-NOV-1996
DEFINITION  Influenza A/Equine/Kentucky/1/94 hemagglutinin (HA1) gene, complete
            cds.
ACCESSION   L39914
VERSION     L39914.1  GI:722403
KEYWORDS    .
SOURCE      Influenza A virus (strain A/equine/Kentucky/1/94)
ORGANISM    Influenza A virus (strain A/equine/Kentucky/1/94)
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1762)
AUTHORS     Daly,J.M., Lai,A.C., Binns,M.M., Chambers,T.M., Barrandeguy,M. and
            Mumford,J.A.
TITLE       Antigenic and genetic evolution of equine H3N8 influenza A viruses
JOURNAL     J. Gen. Virol. 77 (Pt 4), 661-671 (1996)
MEDLINE     96203953
PUBMED      8627254
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JOURNAL      the Western Hemisphere
             Arch. Virol. 146 (6), 1063-1074 (2001)
MEDLINE      21395169
PUBMED       11504416
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AUTHORS      Lai,A.C.K.
TITLE        Direct Submission
JOURNAL      Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma
             State University, 306 Life Science East, Stillwater, OK 74078, USA
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RESULT 4
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LOCUS       AF197247              1061 bp    mRNA        linear    VRL 08-JAN-2003
DEFINITION  Influenza A virus (A/equine/Kentucky/9/95(H3N8)) hemagglutinin
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ACCESSION   AF197247
VERSION     AF197247.1  GI:6651514
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SOURCE      Influenza A virus (A/equine/Kentucky/9/95 (H3N8))
ORGANISM    Influenza A virus (A/equine/Kentucky/9/95 (H3N8))
            viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1061)
AUTHORS     Lai,A.C., Chambers,T.M., Holland,R.E. Jr., Morley,P.S.,
            Haines,D.M., Townsend,H.G. and Barrandeguy,M.
TITLE       Diverged evolution of recent equine-2 influenza (H3N8) viruses in
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DEFINITION    Influenza A virus (A/equine/Kentucky/1/96 (H3N8)) hemagglutinin
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REFERENCE     1  (bases 1 to 1061)
  AUTHORS     Lai,A.C., Chambers,T.M., Holland,R.E. Jr., Morley,P.S.,
              Haines,D.M., Townsend,H.G. and Barrandeguy,M.
  TITLE       Diverged evolution of recent equine-2 influenza (H3N8) viruses in
              the Western Hemisphere
  JOURNAL     Arch. Virol. 146 (6), 1063-1074 (2001)
  MEDLINE     21395169
   PUBMED     11504416
REFERENCE     2  (bases 1 to 1061)
  AUTHORS     Lai,A.C.K.
  TITLE       Direct Submission
  JOURNAL     Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma
              State University, 306 Life Science East, Stillwater, OK 74078, USA
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             precursor (HA1) gene, partial cds.
ACCESSION   AY273168
VERSION   AY273168.1 GI:33415851
KEYWORDS   .
SOURCE   Influenza A virus (A/equine/Oklahoma/2000(H3N8))
  ORGANISM   Influenza A virus (A/equine/Oklahoma/2000(H3N8))
             Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
             Influenzavirus A.
REFERENCE   1 (bases 1 to 1061)
  AUTHORS   Lai,A.C.K., Rogers,K.M., Glaser,A., Tudor,L. and Chambers,T.
  TITLE   Alternate circulation of recent equine-2 influenza viruses (H3N8)
             from two distinct lineages in the United States
  JOURNAL   Virus Res. 100 (2), 159-164 (2004)
   PUBMED   15019234
REFERENCE   2 (bases 1 to 1061)
  AUTHORS   Lai,A.C.K.
  TITLE   Direct Submission
  JOURNAL   Submitted (10-APR-2003) Microbiology & Molecular Genetics, Oklahoma
             State University, 306 Life Science East, Stillwater, OK 74078, USA
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ORIGIN

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1061	100.0	1061	14	AF197241	AF197241 Influenza
2	1056.2	99.5	1061	14	AY273168	AY273168 Influenza
3	1053	99.1	1061	14	AF197248	AF197248 Influenza
4	1051.4	99.1	1061	14	AF197247	AF197247 Influenza
5	1048.2	98.8	1762	14	FLAHAH3B	L39914 Influenza A
6	1043.4	98.3	1060	14	EIVY14059	Y14059 Influenza A
7	1041.8	98.2	1060	14	EIVY14060	Y14060 Influenza A
8	1041.8	98.2	1762	14	FLAHAH3D	L39916 Influenza A
9	1039.2	97.9	1100	14	EIVY14058	Y14058 Influenza A
10	1038.6	97.9	1762	14	FLAHAH3F	L39918 Influenza A
11	1035.4	97.6	1061	14	AF197242	AF197242 Influenza
12	1033.8	97.4	1762	6	BD244631	BD244631 Low tempe
13	1033.8	97.4	1762	6	AR254631	AR254631 Sequence
14	1033.8	97.4	1762	6	AR343239	AR343239 Sequence
15	1033.8	97.4	1762	6	AR455506	AR455506 Sequence
16	1033.8	97.4	1762	14	FLAHAH3A	L39913 Influenza A
17	1032.2	97.3	1762	6	BD244629	BD244629 Low tempe
18	1032.2	97.3	1762	6	AR254629	AR254629 Sequence
19	1032.2	97.3	1762	6	AR343237	AR343237 Sequence
20	1032.2	97.3	1762	6	AR455504	AR455504 Sequence
21	1030.6	97.1	1061	14	AF197245	AF197245 Influenza
22	1030.6	97.1	1762	14	FLAHAH3E	L39917 Influenza A
23	1029	97.0	1061	14	AF197249	AF197249 Influenza
24	1027.4	96.8	1762	14	FLAHAH3C	L39915 Influenza A
25	1022.6	96.4	1061	14	AF197243	AF197243 Influenza
26	1022.6	96.4	1061	14	AF197244	AF197244 Influenza
27	1022.6	96.4	1090	14	EIVY14056	Y14056 Influenza A
28	1022.6	96.4	1762	14	IVAH691	X95637 Influenza A
29	1021.2	96.2	1762	14	IVAH991	X95638 Influenza A
30	1019.4	96.1	1061	14	AY273167	AY273167 Influenza
31	1019.2	96.1	1032	14	IVTAN931	X85088 Influenza A
32	1019.2	96.1	1698	6	AR490205	AR490205 Sequence
33	1019.2	96.1	1698	6	AX018718	AX018718 Sequence
34	1018.4	96.0	1762	6	AR011427	AR011427 Sequence
35	1018.4	96.0	1762	6	I18065	I18065 Sequence 30
36	1016.8	95.8	1762	14	FLAET85HA	M24726 Influenza A
37	1016.2	95.8	1762	14	EIVH3A	L27597 Influenza A
38	1015.6	95.7	1040	14	FLAH3NBHAD	D30680 Influenza A
39	1014.6	95.6	1061	14	AF197246	AF197246 Influenza
40	1014.2	95.6	1099	14	FLAH3NBHAJ	D30686 Influenza A
41	1011.8	95.4	1093	14	FLAH3NBHAE	D30681 Influenza A
42	1010.4	95.2	1762	14	FLAEK87HA	M24728 Influenza A
43	1008.8	95.1	1762	14	FLAEK86HA	M24727 Influenza A
44	1007	94.9	1096	14	FLAH3NBHAG	D30683 Influenza A
45	1006.6	94.9	1060	14	EIVY14057	Y14057 Influenza A

ALIGNMENTS

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RESULT 1
AF197241
LOCUS       AF197241        1061 bp    mRNA    linear   VRL 08-JAN-2003
DEFINITION  Influenza A virus (A/equine/Kentucky/1/98 (H3N8)) hemagglutinin
            precursor (HA1) mRNA, partial cds.
ACCESSION   AF197241
VERSION     AF197241.1  GI:6651502
KEYWORDS    .
SOURCE      Influenza A virus (A/equine/Kentucky/1/98(H3N8))
  ORGANISM  Influenza A virus (A/equine/Kentucky/1/98(H3N8))
            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
            Influenzavirus A.
REFERENCE   1  (bases 1 to 1061)
  AUTHORS   Lai,A.C., Chambers,T.M., Holland,R.E. Jr., Morley,P.S.,
            Haines,D.M., Townsend,H.G. and Barrandeguy,M.
  TITLE     Diverged evolution of recent equine-2 influenza (H3N8) viruses in
            the Western Hemisphere
  JOURNAL   Arch. Virol. 146 (6), 1063-1074 (2001)
  MEDLINE   21395169
  PUBMED    11504416
REFERENCE   2  (bases 1 to 1061)
  AUTHORS   Lai,A.C.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma
            State University, 306 Life Science East, Stillwater, OK 74078, USA
FEATURES             Location/Qualifiers
     source          1..1061
                     /organism="Influenza A virus
                     (A/equine/Kentucky/1/98 (H3N8))"
                     /mol_type="mRNA"
                     /isolate="A/equine/Kentucky/1/98"
                     /db_xref="taxon:217817"
                     /note="H3N8"
     gene            1. .>1061
                     /gene="HA1"
     CDS             30. .>1061
                     /gene="HA1"
                     /codon_start=1
                     /product="hemagglutinin precursor"
                     /protein_id="AAF22345.1"
                     /db_xref="GI:6651503"
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A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24724; GB:J04336; NID:g324014; PIDN:AAA43109.1; PID:g324015
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;18,23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predic·
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:   Length: 565
Score: 9.62e-140   Matches: 324
Percent Similarity: 97.97%   Conservative: 13
Best Local Similarity: 94.19%   Mismatches: 7
Query Match: 92.36%   Indels: 0
                                              Gaps: 0

US-10-826-929A-1 (1-1061) x HMIVE7 (1-565)

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Qy    30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCACC 89
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Db     1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy    90 AGTGGAAACAACACCAGCCACATTATGTCTGGGACACCAGTAGCAAATGAACATTG 149
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Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy   150 GTAAAAACAATAACTGATGACCAAATGAGGTGACAAATGCTACCACTGAATTACTCAGAGC 209
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Db    41 ValLysThrIleThrAspAspGlnIleIleGluValThrAsnAlaThrGluLeuValGlnSer 60

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Db    61 ThrSerIleGlyLysLysCysAsnAsnProTyrArgValLeuAspTyrArgAsnCysThr 80

Qy   270 TTAATAGATGCAATGCCAGGAGACCCCCACTGTGCTTCCAGTATGAGAATTGGAC 329
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Qy   330 CTCTTCATAGAAAGAAGCAGCAGGCGCTTTCAGCAATTGCACCCATATGACATCCCTGACTAT 389
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Qy   390 GCATCGCTCCGGTCCATTGTGACCATCCTCAGGAAACATTAGAATTCAGCAGAGGGATTC 449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy   450 ACATGGACAGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
         ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyGlySerGlyAlaCysArgArgGlySerAlaAsp 160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAATTCGACAACTATACATCTGGGGATTCATCACCCG 629
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy   630 AGCTCAAACCAACAGCAGACAGAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689
         ||||:::|||||||    ::||||||||||:::||||::|||||||||||||||||||||
Db   201 SerThrAsnAsnGluGlnThrLysLeuTyrValGlnLeuLeuGlyArgValThrValSer 220

Qy   690 ACAAAAGAGTCAACAAACCATAGTCCCTATATCGGATCGGATCTGGATAGACCCGGTTAGGGGT 749
         ||||||||||||||||    :::||||||||||||||||::||||||
Db   221 ThrLysArgSerGlnInThrIleIleProAsnIleGlySerArgProValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
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Qy   210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
         ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db    61 IleSerIleGlyLysLysCysAsnAsnProTyrArgValLeuAspTyrArgAsnCysThr 80

Qy   270 TTAATAGATGCAATGCCAGGAGACCCCCACTGTGATGTCTTCCAGTTCCAGTAACAGTCTCA 329
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Db    81 LeuIleAspAlaMetLeuGlyTyrProHisCysAspValPheGlnIleTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAAGAAGCAGCAGGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
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Db   101 LeuPheIleGluArgSerSerThrPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGCTCCGGTCCATTGTGACCATCCTCAGGAACATTACAGCAGAGGGATTC 449
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Qy   450 ACATGGACAGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
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Db   141 ThrTrpThrGlyValThrGlnAsnGlyGlySerGlyAlaCysArgArgGlySerAlaAsp 160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
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Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAATTCGACAACATATACATCTGGGGATTCATCACCCCG 629
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   630 AGCTCAAACCAACAGCAGACAGAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689
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Qy   690 ACAAAAGAGTCAACAAACCATAGTCCCTATATCGGATCGGATCTGGATAGACCCGGTTAGGGGT 749
         |||||||||||||||    :::||||||||||||||||::||||||
Db   221 ThrLysArgSerGlnInThrIleIleProAsnIleGlySerArgProValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGACCATTGTAAAACCTGGAGATATCCTAATGATA 809
         |||||||||||||||||||||||||||||   :::|||||||||||||||::|
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetVal 260

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC 869
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Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGlyLysSer 280

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTACACCCAAAT 929
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Qy   930 GGAAGCATCCCAACGACAAAACCAATTTCAAAATGTGAACAAAGTTACATATGGAAAATGC 989
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Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

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Db   321 ProLysTyrIleLysGlyAsnThrLeuLysTrpProLeuGlyMetArgAsnValProGlu 340

Qy  1050 AAGCAAATCAGA 1061
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Db   341 LysGlnIleLeuArg 344
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Qy  810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC     869
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Qy  870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTCTGAATGTATTACCACCAAT  929
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Db  281 SerIleMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn  300

Qy  930 GGAAGCATCCCCACGACGACAACCATTCAAATGTGAACAAAGTACATATGGAAAATGC    989
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Db  301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyGluCys  320

Qy  990 CCCAAGTATATCAGGCAAAAACACTTAAAGCTGGGATGAGGAATATACCAGAA      1049
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Db  321 ProLysTyrIleLysGlnAsnThrLeuLysLeuGlyMetArgAsnValProGlu       340

Qy  1050 AAGCAAATCAGA   1061
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Db  341 LysGlnIleArg   344
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RESULT 7
HMIVE6
hemagglutinin precursor - influenza A virus (strain A/equine/Fontainebleau/76[H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: F34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: F34064
A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24723; GB:J04336; NID:g323998; NID:g323999; PIDN:AAA43101.1; PID:g323999
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;18,23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predict
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;554,56,/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:

Pred. No.:	1.41e-139	Length:	565
Score:	1764.00	Matches:	325
Percent Similarity:	97.97%	Conservative:	12
Best Local Similarity:	94.48%	Mismatches:	7
Query Match:	92.26%	Indels:	0
DB:	1	Gaps:	0

US-10-826-929A-1 (1-1061) x HMIVE6 (1-565)

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Qy   90 AGTGGAAACAACAGCCACATTATGTCTGGACACCATGCAGTAGCAAATGGAACATTG      149
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Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu  40

Qy  150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC   209
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Qy  270 TTAATAGATGCAATGCTAGGAGACCCCACCTGTGATGGTCTTCCAGTATGAGAATTGGAC  329
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Qy  330 CTCTTCATAGAAAGAACGAGCGCCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT  389
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Db  101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr  120

Qy  390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGACATTAGAAATTCACAGCAGAGGGATTC  449
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Db  121 AlaSerLeuArgSerIleValAlaSerSerGlyAspIleArgAsnSerGlnGlnArgGlyPhe  140

Qy  450 ACATGGCAGGTGTCACTCAAGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGCCGAT   509
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Db  141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysArgArgGlySerAlaAsp  160

Qy  510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAAATCTGAAAACTCTTACCCCACATTGAAT  569
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Db  161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn  180

Qy  570 GTGACAATGCCTACAATAAAAATTTGACAAACTATACATCTCGGGGATTCATCACCCG  629
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Db  181 ValThrMetProAsnAsnAsnAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro  200

Qy  630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA  689
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Db  201 SerThrAsnAsnGluGlnThrLysLeuTyrValGlnGluLysGlyArgValThrValSer  220

Qy  690 ACAAAAGAAGTCAACAAACGATAGTCCCTAAATATGGATCTAGACCGTGGGTAGGGGT  749
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Db  221 ThrLysSerGlnGlnThrIleValProLysTyrGlySerArgProGlyValArgGly  240

Qy  750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA  809
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Db  241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle  260
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RESULT 8
HMIVE5
hemagglutinin precursor - influenza A virus (strain A/equine/New Market/76[H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: E34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: E34064
A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>

A;Cross-references: GB:M24722; GB:J04336; NID:g324010; PIDN:AAA43107.1; PID:g324011
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) #status predicted
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:   Length: 565
Score: 9.78e-138   Matches: 318
Percent Similarity: 97.09%   Conservative: 16
Best Local Similarity: 92.44%   Mismatches: 10
Query Match: 91.11%   Indels: 0
DB: Gaps: 0

US-10-826-929A-1 (1-1061) x HMIVE5 (1-565)

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCAACC   89
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProIle   20

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCATGGCAGTAGCAAATGGAACATTG 149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy 150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy 210 ATTTCAATAGGGAAAATATGCAACACTCATAATAAGTTCTAGATGCGAAGAAAATTGCACA 269
         |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   61 ThrSerIleGlyLysIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr   80

Qy 270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
         |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluLysTrpAsp 100

Qy 330 CTCTTCATAGAAGAAGAGCAGCGCTTTCAGCAATGCTACCCCATATGACATCCCTGACTAT 389
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy 390 GCATCCGCTCCGTCCATTGTGATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AlaSerLeuArgSerIleValAlaSerLeuSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy 450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
         |||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db 141 ThrTrpThrGlyValThrGlnAsnGlyGluSerGlySerAlaCysLysArgGlySerAlaAsp 160

Qy 510 AGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

Qy 570 GTGTCAATGCCTAACAATAAAATTTCGACAACTATACATCTCGGGGATTCATCACCCG 629
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ValThrMetProAsnAsnAsnAsnAspPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy 630 AGCTCAAACCAACAGCAGAGAATTGTACATCCAAGAATCAGGAGGACAGAGTAACAGTCTCA 689
         |||||| |||||| ||||||||||||||||||||||||||||||||||||||||
Db 201 SerThrAsnAspGluGlnThrLysLeuTyrValGlnGluSerGlyArgValThrValSer 220

Qy 690 ACAAAAGAGAGTCAACAAACATGATGACCAAACGATAGACCGTGGGTTAGGGGGT 749
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProValArgGly 240

Qy 750 CAATCAGGCAGGATAGAAGCAGATATACTGGAACTGTAAAACCTGGAGATATCCTAATGATA 809
         ||||||||||||||||||||||||||||||||| ||||||||||||||
Db 241 GlnAlaGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspValLeuMetIle 260

Qy 810 AACAGTAATGCCAACTAGTTGCACCGCCGGGATATTTAAATTGAAAACAGGAGAAAGC 869
         |||||| || ||||||||::::||
Db 261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysMetArgThrGluLysSer 280

Qy 870 TCTGTAATGAGATCAGATGACCATAGACATTGTGTGTCTGAATGTATTACCACCAAAT 929
         |||::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 281 SerIleMetArgSerAspAspHisArgHisCysValSerGluCysIleThrProAsn 300

Qy 930 GGAAGCATCCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATATGAAAAATGC 989
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GlySerIleProAsnAspLysProPheGlnAsnValAlaAsnLysValThrTyrGlyLysCys 320

Qy 990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTTGGCCACTGGGATGAGGAAATATACCAGAA 1049
         ||||||||||||::::|||||||||||::::||||||||||||||||||||||||||
Db 321 ProLysTyrIleLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340

Qy 1050 AAGCAAATCAGA 1061
         ||||||||||||
Db 341 LysGlnIleArg 344

RESULT 9
HMIVE1
hemagglutinin precursor - influenza A virus (strain A/equine/Uruguay/1/63[H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: A34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: A34064
A;Molecule type: genomic RNA
A;Residues: 1-565 <RAW>
A;Cross-references: GB:M24718; GB:J04336; NID:g324024; PIDN:AAA43114.1; PID:g324025
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-551/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:   Length: 565
Score: 6.82e-135   Matches: 1708.00
                                        Matches: 310
Percent Similarity: 95.93%   Conservative: 20
Best Local Similarity: 90.12%   Mismatches: 14
Query Match: 89.33%   Indels: 0
DB: 1   Gaps: 0

US-10-826-929A-1 (1-1061) x HMIVE1 (1-565)

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCAACC   89
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||::
Db   1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValHisSerGlnAsnProIle   20

Qy   90 AGTGGAAACAACACAGCCACATTATGTCTGGGACACCATGGCAGTAGCAAATGGAACATTG 149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 GlyGlyLysAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy 150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy 210 ATTTCAATAGGGAAAATATGCAACACTCATAATAAGTTCTAGATGCGAAGAAAATTGCACA 269
         ||||||||||||| |:::||
Db ...

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C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;18,23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predict
F;29-481,67-292,154-488,296-320/Disulfide bonds: #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:                         Length:        565
Score:                  1699.00    Matches:       309
Percent Similarity:     95.93%     Conservative:   21
Best Local Similarity:  89.83%     Mismatches:     14
Query Match:            88.86%     Indels:          0
DB:                        1       Gaps:            0

US-10-826-929A-1 (1-1061) x HMIVE2 (1-565)
```

```
Qy    30 ATGAAGACAACCATTATTTTGATACTACTGACCCAGTCTGATACTACTGACCAGTCAAAACCAACC 89
         ||||||||||||||||||||||| ::::||||||||||||
Db     1 MetLysThrThrIleLeuIleLeuLeuThrHisTrpValHisSerGlnAsnProThr          20

Qy    90 AGTGGAAACAACACAGCCACCATGTCTCGGGACACCATGCAGTAGCAACATGGAACATTG       149
         |||||||||||||||||||||||
Db    21 GlyGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu        40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC       209
         |||||||||||||||||||||||
Db    41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer        60

Qy   210 ATTTCAATAGGGAAAATATGCAACAACCTATATAAAGTTCTAGATGGAAGAAATGCACA        269
         |||||||||||||||||||||||
Db    61 ThrSerThrGlyLysIleCysAsnAsnProTyrArgValLeuAspGlyArgAsnCysThr        80

Qy   270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC       329
         |||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyAspProHisAsnTyrAspGluAsnTrpAsp               100

Qy   330 CTCTTCATAGAAAGAGCAGCGCTTTCAGGAATTGTCTACCCATATGACATCCCTGACTAT       389
         |||||||||||||||||||||||    :::||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspValProAspTyr       120

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC       449
         ||||||||||||||||||||||| :::||||||||||
Db   121 AlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheMetAlaGluGlyPhe       140

Qy   450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT       509
         |||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyGlySerAlaCysArgArgGlySerAlaAsp          160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAAATAAAAATTTCGACAAAACTATACATCTGGGA       569
         |||||||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuAsnTrpGlnAsnSerGluSerTyrProThrLeuAsn    180

Qy   570 GTGACAATGCCTAACAATAAAAAATTTGACAAACTATACATCTGGGGGGATTCATCACCG       629
         |||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnAspAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro       200

Qy   630 AGCTCAAACCAACACAGCCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA    689
         ||||:::||    :::|||||||:::||||||
Db   201 SerThrAsnAsnGluGlnThrLysLeuTyrValGlnAlaSerGlyArgValThrValSer       220

Qy   690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT       749
         |||||||||||||||||||||||:::||||||
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly       240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA       809
         |||||||||||||||||||||||:::|||
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspValLeuMetIle       260

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTTAAAATGAAAACAGGGAAAAGC       869
         |||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetArgThrGlyLysSer       280

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGGAACATTTGTGTCTGAAATGATTACACCAAAT       929
         |||||||||||||||||||||||    :::||||||
Db   281 SerIleMetArgSerAspAlaProIleGlyThrCysSerSerGluCysIleThrProAsn       300

Qy   930 GGAAGCATCCCCAACGACAAAACCATTTCAAAATGTGACAAAGTTACTATGAAAAATGC       989
         ||||||||||||||||||||||| :::|||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys       320

Qy   990 CCCAAGTATATCAGGCAAAACACTTAAAGCTGGGGATGGAGGAATATACCAGAA        1049
         ||||||||||||||||||||||| :::||||||
Db   321 ProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu       340

Qy  1050 AAGCAAATCAGA                                                     1061
         :::||||||
Db   341 ArgGlnIleArg                                                      344
```

```
RESULT 10
HMIVE2
hemagglutinin precursor - influenza A virus (strain A/equine/Miami/1/63 [H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: B34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: B34064
A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24719; GB:J04336; NID:g324006; PIDN:AAA43105.1; PID:g324007
```

```
Qy   810  AACAGTAATGCCAACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC  869
          ||||||||||||||||::||::|||||||||||||::::||||||||||||||||||||
Db   261  AbnSerAbnGlyAbnLeuIleAlaProArgGlyTyrPheLysMetArgThrGlyLysSer  280

Qy   870  TCTGTAATGAGATCAGATGCAGCACCCATAGACATTTGTGTCTGAATGTATTACACCAAT  929
          ||:::||||||||||::||||:::||||||||||||||||:::|||||||||||||||||
Db   281  SerIleMetArgSerAbpAlaProIleAbpThrCysValSerGluCysIleThrProAbn  300

Qy   930  GGAAGCATCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC  989
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GlySerIleProAbnAbpLysProPheGlnAbnValAbnLysValThrTyrGlyLysCys  320

Qy   990  CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA  1049
          |||||||::|||||:::||||||::||||||||||||||||||||||::||||||||||
Db   321  ProLysTyrValLysGlnSerThrLeuLysLeuLeuThrGlyMetArgAbnValProGlu  340

Qy   1050  AAGCAAATCAGA  1061
           |||||||||||
Db   341  LysGlnIleArg  344
```

RESULT 11
HMIVE4
hemagglutinin precursor - influenza A virus (strain A/equine/Algiers/72[H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: D34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: D34064
A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24721; GB:J04336; NID:g323996; PIDN:AAA43100.1; PID:g323997
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;23,37,53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds; #status predicted
F;554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
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Pred. No.:           1.03e-130       Length:          565
Score:               1658.00         Matches:         299
Percent Similarity:  94.77%          Conservative:    27
Best Local Similarity: 86.92%        Mismatches:      18
Query Match:         86.72%          Indels:          0
DB:                  1               Gaps:            0
```

US-10-826-929A-1 (1-1061) x HMIVE4 (1-565)

```
Qy   30  ATGAAGACAACCATTATTTTGATACTACTACTGGGATGGGTCTACAGTCAAAACCCAACC  89
          ||||||||||||||||||||||||:::::|:|||||||||||||||:::||||||||
Db   1   MetLysThrThrIleIleLeuIleLeuLeuLeuLeuLeuLeuTrpValHisSerGlnIleProIle  20

Qy   90  AGTGTGAAACAACAGCCACCATTATGTCTGGGACAACCATGCAGTAGCAAATGGAACATG  149
          |:||::|:||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21  SerAbpAbnAbnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAbnGlyThrLeu  40

Qy   150  GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC  209
          |||::|||||||||||||||||||||||||:|:||||||||||||||||||||||||||
Db   41  ValLysThrLeuThrAbpAbpGlnThrAbpGluValThrAbnAlaThrGluLeuValGlnSer  60

Qy   210  ATTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAATTGCACA  269
          |||:::|||||||||||:|||||:|||||||||||||::||||||||||||||:||||||
Db   61  ThrSerThrGlyLysIleCysLysAbnProTyrArgValLeuAbpGlyLysAbnCysThr  80
```

```
Qy   270  TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC  329
          ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db   81  LeuIleAbpAlaMetLeuGlyAbpProHisCysAbpValPheGlnTyrGluAbnTrpAbp  100

Qy   330  CTCTTCATAGAAGAAGCAGCGCTTTCAGCAATGCATCCCATAGACATCCCTGACTAT  389
          ||:::||||:::||||||||:::||||||||||||||:|||||||||::||:|||||
Db   101  LeuPheValGluArgSerAlaPheSerAbnCysTyrProTyrAbpValProAbpTyr  120

Qy   390  GCATGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGGAGGATTC  449
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheMetAlaGluGlyPhe  140

Qy   450  ACATGGACAGGTGTCACTCAAAACGGAAGAGTGGACCTGCAACAAAATCTGGAAACTCTG  509
          ||||||||:::||:||||||||:::||||||||||||||||||||||   :||||||||
Db   141  ThrTrpThrGlyValThrGlnAbnGlyArgSerGlyLeuProAbnLysAbn  160
```

```
Qy   510  AGTTCTTTAGGCGACTGAATTGGCTAACAAAATCTGGAAACTCTGGGGATTCATCACCCG  569
          ::||||||:::|||||||||||||::|||||||||::::|||||||||||||||||||||
Db   161  SerPhePheSerArgLeuAbnTrpLeuThrLysSerGluSerSerTyrSerThrLeuAbn  180

Qy   570  GTGACAATGCCTAACAATAAATAAAAATTCGACAAACTATACATCTGGGGATTCATCACCCG  629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ValThrMetProAbnAbnAbpAbnPheAbpPheLysLeuTyrIleTrpGlyIleHisHisPro  200

Qy   630  AGCTCAAACCAACAGCAGAGAATTGTACATCCAGAATCAGGACGAGTAACAGTCTCA  689
          ||:::||:::::|||||||||||::||:||||||||||||||||||||||||||||||
Db   201  SerThrAbnAbnGluGlnThrArgLeuTyrValGlnAlaSerGlyArgValThrValSer  220

Qy   690  ACAAAAGAAGTCAACAAACGATAGTCCCTATATCGGATCGGACCGTGGGTTAGGGGT  749
          ||::|||||||||||||||||||:::||||||||||||||||||||||||||||||
Db   221  ThrLysArgSerGlnLnThrIleLeuProAbnIleGlySerArgProValArgGly  240
```

```
Qy   750  CAATCAGGCAGGATAAGCATATACTGACATTGTAAAACCTGGAGATATCCTAATGATA  809
          ||||||||||||||||||||||||||||||||||::||||||||||||::||||||||
Db   241  GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAbpValLeuValIle  260

Qy   810  AACAGTAATGCCAACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC  869
          ||||||||||||||||||::||::|||||||||||||::::||||||||||||||||||
Db   261  AbnSerAbnGlyAbnLeuIleAlaProArgGlyTyrPheLysMetArgAlaGlyLysSer  280

Qy   870  TCTGTAATGAGATCAGATGCAGCACCCATAGACATTTGTGTCTGAATGTATTACACCAAT  929
          ||:::||||||||||::||||:::||||||||||||||::|||||||||||||||||||
Db   281  SerIleMetArgSerAbpAlaProIleAbpThrCysValPheGluCysIleThrProAbn  300

Qy   930  GGAAGCATCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC  989
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GlySerIleProAbnAbpLysProPheGlnAbnValAbnLysValThrTyrGlyLysCys  320

Qy   990  CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA  1049
          |||||||||::|||::|||||||::||||||||||||||||||||||||::||||||||
Db   321  ProLysTyrValLysGlnSerThrLeuLysLeuLeuAlaThrArgGlyMetArgAbnValProGlu  340

Qy   1050  AAGCAAATCAGA  1061
           ||||:::||||
Db   341  LysGlnIleArg  344
```

RESULT 12
HMIVE3
hemagglutinin precursor - influenza A virus (strain A/equine/Tokyo/71[H3N8])
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C;Accession: C34064
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A;Reference number: A34064; MUID:89204899; PMID:2705299
A;Accession: C34064
A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24720; GB:J04336; NID:g324018; PIDN:AAA43111.1; PID:g324019
C;Genetics:

A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F;535-551/Domain: transmembrane #status predicted <TM1>
F;23,37,53,68,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predict
F;29-481,67-292,79-91,154-488,296-320/Disulfide bonds: #status predicted
F;154,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:   3.28e-130   Length: 565
Score: 1652.00   Matches: 297
Percent Similarity: 94.77%   Conservative: 29
Best Local Similarity: 86.34%   Mismatches: 18
Query Match: 86.40%   Indels: 0
DB: Gaps: 0

US-10-826-929A-1 (1-1061) x HMIVE3 (1-565)

Qy   30 ATGGAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCAACC   89
          |||||||||| ||||||||||||| ||||||||||||| ||::|||||| ||||
Db   1 MetLysThrThrThrIleLeuIleLeuThrHisTrpValHisSerGlnIleProIle   20

Qy   90 AGTGGAAACAACACAGCCACCATATGTCTGGACACCATGAGCAGTAGCAAATGGAACATTG 149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 AsnAsnAsnThrAlaThrHisCysLeuGlyHisHisAlaAlaAsnGlyThrLeu   40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTACTGAATTAGTTCAGAGC 209
          ||::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrLeuThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy   210 ATTTCAATAGGGAAAATGCAACAACTCATATAAGTTCTAGATGGAAGAAATTGCACA   269
          |||| ||||||||||||||||||||||||||||||||||::||||||||||||
Db   61 ThrSerThrGlyLysMetGlnGlnLeuIleLysSerArgValLeuValLeuAspGlyLysAsnCysAsnThr 80

Qy   270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
          ::: ||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAAGAAGCAGCGCCTTCAGCAATGCTACCACCAATGACATCCCCGACTAT 389
          || |||||||||||||||||||||||||||:::||||||||||||||:||:|:|:||||
Db   101 LeuPheValGluArgSerSerAlaPheSerAsnAlaThrThrAsnAspIleProAsnTyr 120

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACACGCAGAGGATTC 449
          ||| ||||||||||||||||||||||||||||||:::|||||||||||||||||
Db   121 AlaLeuLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrArgArgGlyPhe 140

Qy   450 ACATGGACAGGTGTCACTCAAACGGAGAAGTGGAGCTGCAAAAGGGGATCAGCCGAT   509
          |||||||||| ||| ||| ||||||||||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyGlySerSerSerCysArgArgGlySerAlaAsp 160

Qy   510 AGTTTCTTTAGCCCACTGAATTGGCTAACAAAATCGGAAACTCTTACCCCACCATTGAAT 569
          ||||||| ||||||||||||||||||||||||||||||::|||||| ||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGluThrLeuThrProProLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAAATTCGACAACTATACATCTGGGGGATTCATCACCCG   629
          |||||||||||||||||||||||||||||||::||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnAsnAspAsnPheAspLysLeuTyrValTrpGlyIleHisHisPro 200

Qy   630 AGCTCAAACCAACAGCAGACAGATTGTACATCCAAGAATCAGGACGCGAGTAACAGTCTCA 689
          || |||||||||||||||||||||||||||||||||::|||||||||||||||||||||
Db   201 SerThrAsnAsnGluGlnThrLysLeuTyrValGlnAlaSerGlyArgValThrValSer 220

Qy   690 ACAAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT   749
          |||| |||||||||||||||||||||||||||||::::||||||||||||||||
Db   221 ThrLysArgSerGlnGlnThrIleValProAsnIleGlyLeuArgProTrpValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGAAGATATCCTAATGATA 809
          |||||||||||||:::|||||||||||||||||||||||||||||::|||||||||
Db   241 GlnSerGlyArgValSerIleTyrTrpThrIleValLysProGluAspIleLeuMetIle 260

Qy   810 AACAGTAATGGCAACTAGTTGCACCGCGGGATATTTAAATTGAAACAGGGAAAAGC 869
          |||||||||||||||||::::|||||| |||::::||||||:||::||||::||
Db   261 AsnSerAsnGlyAsnLeuLeuAlaProArgGlyTyrPheLysIleArgAlaGlyLysSer 280

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACATTGTGTGTCTGAATGTATTACCACCAAAT 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 SerIleMetArgSerAspAlaProIleAspIleValCysLeuAsnValLeuThrProAsn 300

Qy   930 GGAAGCATCCCCACGACAACAACCATTCAAAATGTGAACAAAGTGACACATATGAAAATGC 989
          |||||||||||||||||||||||||||||||||||||||||||||::||||||||||||
Db   301 GlySerIleProAlaAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyLysCys 320

Qy   990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGAATATACCAGAA 1049
          ||||||||::::||||||||||||||||::||||||||||||||||||||||||||
Db   321 ProLysTyrValLysGlnThrLeuLysLeuAlaThrGlyMetArgAsnIleProGly   340

Qy 1050 AAGCAAATCAGA 1061
          |||::::||||
Db   341 LysArgLeuArg   344

RESULT 13
HMIVDU
hemagglutinin precursor - influenza A virus (strain A/duck/Ukraine/63)
C;Species: influenza A virus
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 28-May-1999
C;Accession: A04053
R;Fang, R.; Min Jou, W.; Huylebroeck, D.; Devos, R.; Fiers, W.
Cell 25, 315-323, 1981
A;Title: Complete structure of A/duck/Ukraine/63 influenza hemagglutinin gene: animal vi
A;Reference number: A04053; MUID:82025542; PMID:6169439
A;Accession: A04053
A;Molecule type: genomic RNA
A;Residues: 1-566 <FAN>
A;Cross-references: GB:V01087; GB:J02109; NID:g60756; PIDN:CAA24271.1; PID:g60757
C;Superfamily: influenza virus hemagglutinin
C;Keywords: hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F;346-566/Product: hemagglutinin HA2 #status predicted <HA2>
F;536-552/Product: transmembrane #status predicted <TM1>
F;30-482,68-293,80-92,155-489,297-321/Disulfide bonds: #status predicted
F;555,562,565/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:   4.71e-121   Length: 566
Score: 1542.50   Matches: 278
Percent Similarity: 90.14%   Conservative: 33
Best Local Similarity: 80.58%   Mismatches: 33
Query Match: 80.67%   Indels: 1
DB: Gaps: 1

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Qy   30 ATGGAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAAC---CCA 86
          |||||||||| ||||||||||||| |||||||||:: ||:::||||||
Db   1 MetLysThrValIleLeuAlaLeuSerTyrIleLeuCysLeuThrPheGlyGlnAspLeuPro 20

Qy   87 ACCAGTGGAAACAACACAGCCACCATATGTCTGGACACCAGTAGCAAATGGAACA   146
          ::: |||| |||:||||:::|||||||||||||||||| |||:||||
Db   21 GlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGlyThr   40

Qy   147 TTGGTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAG 206
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 IleValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGln 60

Qy   207 AGCATTTCAATAGGGAAAATGCAACAACTCATATAAGTTCTAGATGGAAGAAATTGC 266
          ||||::::|||||||||||||||||||||||||||||::::::|||||||||||||
Db   61 SerSerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyArgAlaCys 80

Qy   267 ACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGG 326
          ||||||::::|||||||||||||||||||||||||||||||||||||::||||||||
Db   81 ThrLeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnAsnGluThrTrp 100

F;520-536/Domain: transmembrane #status predicted <TM1>
F;8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted
F;539,546,549/Binding site: palmitate (Cys) (covalent) #status predicted

Alignment Scores:
Pred. No.:   1.12e-120   Length: 550
Score: 1538.00   Matches: 274
Percent Similarity: 92.94%   Conservative: 29
Best Local Similarity: 84.05%   Mismatches: 23
Query Match: 80.44%   Indels: 0
DB: 1   Gaps: 0

US-10-826-929A-1 (1-1061) x HMIV89 (1-550)

```
Qy    84 CCAACCAGTGGAAACAACACAGCCACCATTAGTCTCGGGACACCAGTAGCAGTAGCAAATGGA 143
             |||   ||:||||||||||||||||||||||||||||||||:|||||||:||||||||||
Db     4 ProGlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGly  23

Qy   144 ACATTGTAAAACAATAACTGATGACCAAATTGAGCGACAAATGCTACTGAATTAGTT 203
            :|||||||||||:|||||||||||||||||||||||||||||:|||||||:||||||
Db    24 ThrIleValLysThrIleThrAspAspGlnIleGluValThrArgAsnAlaThrGluLeuVal  43

Qy   204 CAGAGCATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTCAGATGGAAGAAAT 263
            |||||||||||||||||         :::|||||||:::::|||||||||||||||||||
Db    44 GlnSerSerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyArgAsp  63

Qy   264 TGCACATTAATAGATGCAATGCTAGGAGCACCCCACTGTGATGTCTTCCAGTATGAGAAT 323
            |||||||||||||:||||||||||:::|||||||||||||||||||||||||||||||||
Db    64 CysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspValPheGlnTyrGluThr  83

Qy   324 TGGGACCTCTTCATAGAAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATAGACATCCCT 383
            |||||||||||||||||||||||||||||:||||||||||||:||||||:::|||||||||
Db    84 TrpAspLeuPheValGluArgSerAsnAlaPheSerAsnCysTyrProTyrAspValPro 103

Qy   384 GACTATGCCATGCTGCTCCGGTCCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAG 443
            ||||||||||||||||||||||||||||:|:|||||||||||||||||:|||||||||||
Db   104 AspTyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleThrGlu 123

Qy   444 GGATTCACATGGACAGGTGTCACTCAAAATGGAAGAGAGTGGAGCCTGCAAAAGGGGATCA 503
            ||||||||||||:||||||||||||:||||||||||||||||:||||||:||||||||:||
Db   124 GlyPheThrTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyPro 143

Qy   504 GCCGATAGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACCA 563
            |||||||||||||||||||||||||||||||||||||||||||:||||::|||||||||||
Db   144 AlaSerGlyPhePheSerArgLeuAsnTrpLeuThrLysSerGlySerThrTyrProVal 163

Qy   564 TTGAAATGTGACAATGCCTAACAATAAAAATTTGACAAACTATACATCTGGGGGATTCAT 623
            |||||||||||||||||||::|||||||||||||:|:||||||||||||||||||||||||
Db   164 LeuAsnValThrMetProAsnAspAsnPheAspAsnLeuTyrValGlnAlaSerGlyArgValThr 203

Qy   624 CACCCGAGCTCAAACCACCAGACAGAAATTGTACATCCAAGAATCAGGACGAGTAACA 683
            ||||||||||||||||||:|||||||||||||||||||||||||||:|||||||||||
Db   184 HisProSerThrAsnGlnGluGlnThrAsnLeuTyrValGlnAlaSerGlyArgValThr 203

Qy   684 GTCTCAACAAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTT 743
            ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db   204 ValSerThrArgArgSerGlnInThrIleIleProAsnIleGlySerArgProTrpVal 223

Qy   744 AGGGGTCAATCAGGCAGGATAAGCATAGACATTGTAAAACCTGGAGATATCCTA 803
            ||||||||||||||||:||||| |||||||||||:|||||||||||||||||||:||
Db   224 ArgGlyGlnSerGlyArgIleSerIleAspIleValLysProGlyAspIleLeu 243

Qy   804 ATGATAAACAGTAATGGCAACTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGG 863
            ::|||||||||||||||||||||||||||||||||:|||||||:||||||||||||||||
Db   244 ValIleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetArgThrGly 263

Qy   864 AAAAGTCTCTGTAATGAAGATCATGATGCCACCCATAGACATTTGTGTGTCTGAATGTATTACA 923
            |||||:::||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db   264 LysSerSerValMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThr 283

Qy   924 CCAAATGGAAGCATCCCCAACGACAAACCATTCAAAATGCAAGAAGTTACATATGGA 983
            ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
```

Qy   327 GACCTCCTCATAGAAAAGAAGCAGCGCCTTTCAGCAATTGCTACCCATAGACATCCTGAC 386
            |||||||||:|||||||||||||||||||||||||||||||||:|||||||||||||||
Db   101 AspLeuPheValGluArgSerAsnAlaPheSerAsnCysTyrProTyrAspValProAsp 120

Qy   387 TATGCCATGCTGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGA 446
            ||||||||||||||||||::|||||||||||||||||||||||||||||:||||||||||
Db   121 TyrAlaSerLeuArgSerLeuValAlaSerSerGlyThrLeuGluPheIleThrGluGly 140

Qy   447 TTCACATGGACAGGTGTCACTCAAAACGGAAGAGAGTGGAGCCTGCAAAGGGGATCAGCC 506
            |||||||||:||||||||||||||||:||||||||||||||:||||||||:|||||||||
Db   141 PheThrTrpThrGlyValThrGlnAsnGlyGlySerAsnAlaCysLysArgGlyProAla 160

Qy   507 GATAGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACCATTG 566
            :::||||||||||||||| :::::||||||||||||||||||||||||||||| |||
Db   161 AsnGlyPhePheSerArgLeuAsnTrpLeuThrLysSerGluSerAlaTyrProValLeu 180

Qy   567 AATGTGACAATGCCTAACAATAAAAATTTGACAACTATACATCATCTGGGGATTCATCAC 626
            ||||||||||||||||||||:||||||||||:|||||||||||||||||||||||||||||
Db   181 AsnValThrMetProAsnAsnAspAsnPheAspLysLeuTyrIleTrpGlyValHisHis 200

Qy   627 CCGAGCTCAAACCACCAGACAGCAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTC 686
            |||||||||||||||:||||||:|||||||||||||||||||||||||:||||||||||||
Db   201 ProSerThrAsnGlnGlnThrAsnLeuTyrValGlnAlaSerGlyArgValThrVal 220

Qy   687 TCAACAAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGATCCGTGGTTAGG 746
            ||||||:||||||||||||||||||||||||||||||||||||:|||||:|||||||||||
Db   221 SerThrArgArgSerGlnInThrIleIleProAsnIleGlySerArgProValArg 240

Qy   747 GGTCAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATG 806
            ||||||||||||||||||||||:|||||||||||||:|||||||||||||||||||||||
Db   241 GlyGlnProGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuVal 260

Qy   807 ATAAACAGTAATGGCAACTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGAAA 866
            |||||||||||||||:||||||||||||||||||:|||||:||||||||||||||
Db   261 IleAsnSerAsnGlyAsnLeuIleAlaProArgGlyTyrPheLysMetArgThrGlyLys 280

Qy   867 AGCTCTGTAATGAGATCAGATGCCACCCATAGACATTTGTGTCTGAATGTATTACCA 926
            ||||:::|||||||||||||||||||||||:||||||||||||:|||||||:||||||
Db   281 SerSerIleMetArgSerAspAlaProIleAspThrCysValSerGluCysIleThrPro 300

Qy   927 AATGGAAGCATCCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAA 986
            ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||::||
Db   301 AsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGlyAla 320

Qy   987 TGCCCCAAGTATATCAGGCAAAACACTTTAAAGCTGGATGAGGAATATACCA 1046
            |||||:::||||||:|||||||:||||||||||||||||||:||||||::|||
Db   321 CysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValPro 340

Qy 1047 GAAAAGCAAATCAGA 1061
            ||||||||||| |||
Db   341 GluLysGlnThrArg 345

RESULT 14
HMIV89
hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/7/82) (fragment)
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: D27813
R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G.
Virology 159, 109-119, 1987
A;Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks.
A;Reference number: A94363; MUID:87265458; PMID:2440178
A;Accession: D27813
A;Molecule type: genomic RNA
A;Residues: 1-550 <KID>
A;Cross-references: GB:M16740; NID:g324087; NID:g324088; PIDN:AAA43146.1; PID:g324088
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-328/Product: hemagglutinin HA1 #status predicted <HA1>
F;330-550/Product: hemagglutinin HA2 #status predicted <HA2>

```
Db   284  ProAsnGlySerIleProAsnAspLysProPheGlnAsnValAsnLysIleThrTyrGly  303

Qy   984  AAATGCCCCAAGTATATCAGGCAAAACACTTAAAGCTGGCCACTGGGATGAGGAATATA 1043
          ||||||||:::||||||||||||||||||||||||:|||||:||||||||||||:::
Db   304  AlaCysProLysTyrValLysGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnVal  323

Qy  1044  CCAGAAAAGCAAATCAGA 1061
          |||||||||||||  |||
Db   324  ProGluLysGlnThrArg  329


RESULT 15
HMIV15

hemagglutinin precursor - influenza A virus (strain A/duck/Hokkaido/10/85)  (fragment)
N;Contains: hemagglutinin HA1; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: G27813
R;Kida, H.; Kawaoka, Y.; Naeve, C.W.; Webster, R.G.
Virology 159, 109-119, 1987
A;Title: Antigenic and genetic conservation of H3 influenza virus in wild ducks.
A;Reference number: A94363; MUID:87265458; PMID:2440178
A;Accession: G27813
A;Molecule type: genomic RNA
A;Residues: 1-550 <KID>
A;Cross-references: GB:M16743; NID:g324093; NID:g324092; PIDN:AAA43149.1; PID:g324094
C;Genetics:
A;Map position: segment 4
C;Superfamily: influenza virus hemagglutinin
C;Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F;1-328/Product: hemagglutinin HA1 #status predicted <HA1>
F;330-550/Product: hemagglutinin HA2 #status predicted <HA2>
F;520-536/Domain: transmembrane #status predicted <TM1>
F;8,22,38,165,285,483/Binding site: carbohydrate (Asn)  (covalent) #status predicted
F;14-466,52-277,64-76,139-473,281-305/Disulfide bonds: #status predicted
F;539,546,549/Binding site: palmitate (Cys)  (covalent) #status predicted

Alignment Scores:
Pred. No.:                                      Length:      550
Score:             1537.00                       Matches:     272
Percent Similarity: 92.94%                       Conservative: 31
Best Local Similarity: 83.44%                    Mismatches:  23
Query Match:       80.39%                         Indels:      0
DB:                1                              Gaps:        0

US-10-826-929A-1 (1-1061) x HMIV15 (1-550)

Qy    84  CCAACCAGTGGAAACAACAACAGCCACCATTATGTCTGGGACACCATGCAGTAGCAAATGGA  143
             |||      ||:::       ||||||||||||||||||||||||||||||||||||
Db     4  ProGlyAsnAspAsnSerThrAlaThrLeuCysLeuGlyHisHisAlaValProAsnGly   23

Qy   144  ACATTGGTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTT  203
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    24  ThrLeuValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuVal   43

Qy   204  CAGAGCCATTCAATAGGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAAT  263
          |||||                    ::::::|||||||||||||:::||||||||||:
Db    44  GlnSerSerThrGlyLysIleCysAsnAsnProHisArgIleLeuAspGlyArgAsp     63

Qy   264  TGCACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAAT  323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    64  CysThrLeuIleAspAlaLeuLeuGlyAspProHisCysAspValPheGlnValAspThr   83

Qy   324  TGGGACCCTCTCATGAAGAAAGAAGCAGCGCGTTCAGCAATTGCTACCATATGACATCCCT  383
          |||||||||||||||||||||||||||||||||||||||:||||:||||||||||||:::
Db    84  TrpAspProLeuValGluArgGlnAlaPheSerAsnCysTyrProTyrAspValPro     103

Qy   384  GACTATGCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAG  443
          |||||||||||||||||||::||:|||||||||||||||||||||||||||||||||  ||
Db   104  AspTyrAlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheIleThrGlu  123

Qy   444  GGATTCACATGGACAGGTGTCACTCAAAACGGAGAAGTGCAGCCTGCAAAAGGGGATCA  503
          |||||||||||||||||:|:||||||||||||||||||:||||||||||||::::
Db   124  GlyPheThrTrpThrGlyValThrGlnThrGlyGlySerAsnAlaCysLysArgGlyPro  143
```

```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:      February 27, 2005, 18:07:19 ; Search time 217 Seconds
                                     (without alignments)
                              5007.521 Million cell updates/sec

Title:       US-10-826-929A-1
Perfect score: 1912
Sequence:    1 agcaaaagcagggatatt.........taccagaaaagcaaatcaga 1061

Scoring table: BLOSUM62
             Xgapop   10.0 , Xgapext   0.5
             Ygapop   10.0 , Ygapext   0.5
             Fgapop    6.0 , Fgapext   7.0
             Delop     6.0 , Delext    7.0

Searched:    1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:        3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10826929/runat_27022005_095242_27584/app_query.fasta_1.1223
-DB=UniProt_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10826929 @CGN_1_1_244 @runat_27022005_095242_27584 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   UniProt_03
             1: uniprot_sprot;*
             2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1836	96.0	344	2	Q9Q6P2	Q9q6p2 influenza a
2	1832	95.8	344	2	Q6WRT8	Q6wrt8 influenza a
3	1831	95.8	344	2	Q82846	Q82846 influenza a
4	1831	95.8	565	2	Q67103	Q67103 influenza a
5	1827	95.6	344	2	Q9Q6N5	Q9q6n5 influenza a
6	1827	95.6	344	2	Q9Q6N6	Q9q6n6 influenza a
7	1822	95.3	346	2	O56857	O56857 influenza a
8	1822	95.3	346	2	O56858	O56858 influenza a
9	1816	95.0	565	2	Q67105	Q67105 influenza a
10	1813	94.8	362	2	Q9YJV1	Q9yjv1 influenza a
11	1813	94.8	565	2	Q67102	Q67102 influenza a
12	1813	94.8	565	2	Q67107	Q67107 influenza a
13	1812	94.8	344	2	Q9Q6P1	Q9q6p1 influenza a
14	1810	94.7	565	2	Q67106	Q67106 influenza a
15	1808	94.6	344	2	Q9Q6N8	Q9q6n8 influenza a
16	1808	94.6	565	2	Q82793	Q82793 influenza a
17	1806	94.5	344	2	Q82843	Q82843 influenza a
18	1806	94.5	344	2	Q9Q6N7	Q9q6n7 influenza a
19	1806	94.5	565	1	HEMA_IAHTE	HEMA_IAHTE influenza a
20	1805	94.4	565	1	HEMA_IAHK7	P16996 influenza a
21	1804	94.4	565	2	Q67104	Q67104 influenza a
22	1803	94.3	343	2	Q9YJV7	Q9yjv7 influenza a
23	1803	94.3	344	2	Q9Q6P0	Q9q6p0 influenza a
24	1803	94.3	362	2	Q9YJV6	Q9yjv6 influenza a
25	1803	94.3	363	2	Q9YJV4	Q9yjv4 influenza a
26	1799	94.1	357	2	O56856	O56856 influenza a
27	1798	94.0	344	2	Q6WRT9	Q6wrt9 influenza a
28	1798	94.0	354	2	O12292	O12292 influenza a
29	1797	94.0	344	2	Q9Q6N4	Q9q6n4 influenza a
30	1797	94.0	344	2	Q9Q6N9	Q9q6n9 influenza a
31	1795	93.9	353	2	O12294	O12294 influenza a
32	1795	93.9	362	2	Q9YJV9	Q9yjv9 influenza a
33	1795	93.9	565	1	HEMA_IAHSU	Q08011 influenza a
34	1794	93.8	565	1	HEMA_IAHK6	P19699 influenza a
35	1794	93.8	565	2	Q82792	Q82792 influenza a
36	1786	93.4	344	2	Q82844	Q82844 influenza a
37	1786	93.4	565	2	Q6txb8	Q6txb8 influenza a
38	1785	93.4	346	2	O56855	O56855 influenza a
39	1784	93.3	344	2	Q82848	Q82848 influenza a
40	1784	93.3	360	2	Q9YJV8	Q9yjv8 influenza a
41	1781	93.1	359	2	Q9YJV5	Q9yjv5 influenza a
42	1779	93.0	565	2	Q66752	Q66752 influenza a
43	1778	93.0	565	2	Q82559	Q82559 influenza a
44	1776	92.9	344	2	Q82847	Q82847 influenza a
45	1775	92.8	344	2	Q82845	Q82845 influenza a

```
                              ALIGNMENTS

RESULT 1
Q9Q6P2
ID   Q9Q6P2;                PRELIMINARY;       PRT;      344 AA.
AC   Q9Q6P2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor (Fragment).
GN   Name=HA1;
OS   Influenza A virus (A/equine/Kentucky/1/98(H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=217817;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21395169; PubMed=11504416;
RA   Lai A.C., Chambers T.M., Holland R.E. Jr., Morley P.S., Haines D.M.,
RA   Townsend H.G., Barrandeguy M.;
RT   "Diverged evolution of recent equine-2 influenza (H3N8) viruses in the
RT   Western Hemisphere.";
RL   Arch. Virol. 146:1063-1074(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lai A.C.K.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; AF197241; AAF22345.1; -.
DR   HSSP; P03437; 2VIU.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
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DR   ProDom; PD000225; Hemagglutin; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL        1     15       Potential.
FT   CHAIN        16   >344       hemagglutinin.
FT   NON_TER     344    344
SQ   SEQUENCE    344 AA;  38280 MW;  D5A49D574FB785ED CRC64;

Alignment Scores:
Pred. No.:              1.51e-148        Length:          344
Score:                  1836.00          Matches:         344
Percent Similarity:     100.00%          Conservative:      0
Best Local Similarity:  100.00%          Mismatches:        0
Query Match:            96.03%           Indels:            0
DB:                                      Gaps:              2

US-10-826-929A-1 (1-1061) x Q9Q6P2 (1-344)

Qy    30 ATGAAGACAACCATTATTTGATACTACTGACCATTGGGTCTCACAGTCAAAACCCAACC      89
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetLysThrThrIleIleLeuIleLeuThrHisTrpValTyrSerGlnAsnProThr      20

Qy    90 AGTGGAAACAACAGCCACCATTATGTCTGGGACACCATTGGGTTCAGTAGCAAATGGAACATTG     149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAlaAsnGlyThrLeu      40

Qy   150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC     209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer      60

Qy   210 ATTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA     269
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 IleSerIleGlyLysIleCysAsnAsnSerTyrLysValLeuAspGlyArgAsnCysThr      80

Qy   270 TTAATAGATGCAAATGCTAGAGAGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC     329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaAsnAlaMetLeuGlyAspThrHisGlnPheValPheGlnPheGlnPheProAsp     100

Qy   330 CTCTTCATAGAAGAAGAGCAGCGCTTTCAGCAATGCTACCCATATGACATCCCTGACTAT     389
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr     120

Qy   390 GCATCGCTCCGGTCCCATTGTAGCATCCTCAGGAACCATTAGAATTCACAGCCAGAGGATTC     449
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGlePheThrAlaGluGlyPhe     140

Qy   450 ACATGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT     509
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrTrpTrpThrGlyValThrGlnAsnGlyGluSerGlyAlaCysLysArgGlySerAlaAsp     160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGAAAACTCTTACCCACATTGAAT     569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGluAsnSerTyrProThrLeuAsn     180

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAACAATACATCTGGGGGATTCATCACCCG     629
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysAsnThrSerGlyIleIleTrpGlyIleIleHisHisPro     200

Qy   630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAGCGAGTAACAGTCTCA     689
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 SerSerAsnGlnGlnGlnThrGluLeuTyrIleGlnGluSerGlySerGlyValArgThrValSer     220

Qy   690 ACAAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGGTTAGGGGT     749
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 ThrLysArgGluSerGlnInThrIleValProAsnIleGlySerArgProTrpValArgGly     240

Qy   750 CAATCAGGCAGGGAGATAAGCATAACTGGGACCATTGTAAAACCTGGAGATATCCTAATGATA     809
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GlnSerGlyArgGluSerIleSerIleThrGlyThrIleValLysProGlyAspIleLeuMetIle     260

Qy   810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC     869
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuValAlaLeuAsnLeuAsnLeuGlyAsnThrValIleLysSerTyrSer     280
```

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Qy   870 TCTGTAAATGAGATCAGATGCACCCATAGACATTGTGTCTGAATGATTATTACCACCAAAT     929
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 SerValMetArgSerAspAlaProIleAspIleValSerGluCysValSerThrProAsn     300

Qy   930 GGAGGCATCCCACGACGACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC     989
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys     320

Qy   990 CCCAAGTATATCAGGCAAAACACTTAAAGCTGGCCACTGGCATGAGGAGAATATACCAGAA     1049
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgArgAsnIleProGlu     340

Qy  1050 AAGCAAATCAGA     1061
         ||||||||||||
Db   341 LysGlnIleArg     344
```

```
RESULT 2
Q6WRT8
ID   Q6WRT8            PRELIMINARY;     PRT;    344 AA.
AC   Q6WRT8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hemagglutinin (Fragment).
GN   Name=HA1.
OS   Influenza A virus (A/equine/Oklahoma/2000(H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=241186;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15019234; DOI=10.1016/j.virusres.2003.11.019;
RA   Lai A.C.K., Rogers K.M., Glaser A., Tudor L., Chambers T.;
RT   "Alternate circulation of recent equine-2 influenza viruses (H3N8)
RT   from two distinct lineages in the United States.";
RL   Virus Res. 100:159-164(2004).
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; AY273168; AAQ18435.1; -.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin.
FT   NON_TER     344    344
SQ   SEQUENCE    344 AA;  38281 MW;  D5ACB577479FA5ED CRC64;

Alignment Scores:
Pred. No.:              3.33e-148        Length:          344
Score:                  1832.00          Matches:         343
Percent Similarity:     100.00%          Conservative:      1
Best Local Similarity:  99.71%           Mismatches:        0
Query Match:            95.82%           Indels:            0
DB:                                      Gaps:              0

US-10-826-929A-1 (1-1061) x Q6WRT8 (1-344)

Qy    30 ATGAAGACAACCATTATTTGATACTACTGACCATTGGGTCTCACAGTCAAAACCCAACC      89
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetLysThrThrIleIleLeuIleLeuThrHisTrpValTyrSerGlnAsnProThr      20

Qy    90 AGTGGAAACAACAGCCACCACATTATGTCTGGGACACCAGTAGCAAGATTG     149
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAlaAsnGlyThrLeu      40
```

```
OS   Influenza A virus (A/eq/Newmarket/93/(H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=159470;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/eq/Newmarket/93;
RX   MEDLINE=96203953; PubMed=8627254;
RA   Daly J.M., Lai A.C., Binns M.M., Chambers T.M., Barrandeguy M.,
RA   Mumford J.A.;
RT   "Antigenic and genetic evolution of equine H3N8 influenza A viruses.";
RL   J. Gen. Virol. 77:661-671(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/eq/Newmarket/93;
RA   Yates P.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; X85088; CAA59415.3; -.
DR   HSSP; P03437; 2VIU.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin.
FT   NON_TER      344    344
SQ   SEQUENCE   344 AA;   38308 MW;  214E096F59F73510 CRC64;
```

```
Alignment Scores:
Pred. No.:
Score:                   4.06e-148           Length:              344
                         1831.00             Matches:             341
Percent Similarity:      100.00%             Conservative:        3
Best Local Similarity:   99.13%              Mismatches:          0
Query Match:             95.76%              Indels:              0
DB:                                          Gaps:                0
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US-10-826-929a-1 (1-1061) x Q82846 (1-344)

Qy   30 ATGAAGACAACAACCATTATTTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCACC 89
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy   90 AGTGGAAACAACACAGCCACCATTATGTCTGGGACACCAGTAGCAAATGGAACATTG 149
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy  150 GTAAAAACAATAACTGATGACCAAATTGAGTGACAAATGCTACTGAATTAGTTCAGAGC 209
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy  210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCAGATGGAAGAAATTGCACA 269
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr 80

Qy  270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGATGTCTTCCAGTATGGAATTGGGAC 329
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp 100

Qy  330 CTCTTCATAGAAGGAGCAGCGGCTTTCAGCAATTGCTACCATATGACATCCCTGACTAT 389
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 LeuPheIleGluGlyArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy  390 GCATCGCTCCGGTCCATTGTAGCATCCTCCAGGAACATTAGAATTCACAGCAGAGGATTC 449
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy  450 ACATGACAGAGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 ThrTrpThrGlyValThrGlnAsnGlyGlySerGlyAlaCysLysLysGlySerAlaAsp 160

Qy  510 AGTTCCTTAGCCGACTGAATTGGCTAACAAAATCGGAAACTCTTACCCCACATTGAAT 569
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

Qy  570 GTGACAATGCCTAACAATAAAAATTCGACAAACTATACATCTGGGGGATTCATCACCCG 629
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy  630 AGCTCAAACCAACAGCAGACAGAATTGTCATCCCAAGAATCAGGAGCAGTAACAGTCTCA 689
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 SerSerAsnGlnGlnGlnThrGluLeuTyrIleGlnGluSerGlyArgValThrValSer 220

Qy  690 ACAAAAAGAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT 749
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  221 ThrLysArgSerGlnThrGlnThrIleValProAsnIleGlySerArgProValValArgGly 240

Qy  750 CAATCAGGCGAGGATAAGCATATACTGGACCCATTGTAAAACCTGGAGATATCCTAATGATA 809
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

Qy  810 AACAGTAATGCAACTAGTTGCACCGCGGGATATTTTAAATTGAAAACAGGGAAAAGC 869
            ||||||||||||||||||||||||||||||||||||||||||||||||||::::|
Db  261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280

Qy  870 TCTGTAATGACGATCAGATGCACCCCATAGACATTTGTGTCTGAATGTATTACCACCAAAT 929
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 SerValMetThrSerAspAlaProIleAspThrCysIleSerGluCysIleThrProAsn 300

Qy  930 GGAAGCATCCCAACGACAAACCATTCAAATGAACAAAGTTACATATGGAAAATGC 989
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GlySerIleProAsnAspAspLysProLysSerGlyGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy  990 CCCAAGTATATCAGGCAAAACACTTTAAAGTGGCCACTGGGATGAGGAGGATATACCAGAA 1049
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnIleProGlu 340

Qy 1050 AAGCAAATCAGA 1061
            ||||||||||||
Db  341 LysGlnIleArg 344
```

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RESULT 3
Q82846
ID   Q82846      PRELIMINARY;      PRT;   344 AA.
AC   Q82846;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   HA0 subunit of haemagglutinin (Fragment).
GN   Name=HA1;
```

```
DR   HSSP; P03437; 1QU1.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN2.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL        1     15       Potential.
FT   CHAIN        16    344       hemagglutinin.
FT   CHAIN        16    565       hemagglutinin.
SQ   SEQUENCE   565 AA;  63714 MW;  01FF3B99A7407105 CRC64;

Alignment Scores:
Pred. No.:                           Length:         565
Score:                4.33e-148      Matches:        341
Percent Similarity:   100.00%        Conservative:     3
Best Local Similarity: 99.13%        Mismatches:       0
Query Match:           95.76%        Indels:           0
DB:                    2             Gaps:             0

US-10-826-929a-1 (1-1061) x Q67103 (1-565)

Qy    30 ATGGAGACAACCATTATTTGATACTACTACTTGATCCAGTCAGTAAAACCCAACC 89
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetLysThrThrIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr 20

Qy    90 AGTGGAAACAACAGCCACCATATGTCTCGGACACCATGCAGTAGCAAATGGAACATTG 149
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAlaAsnGlyThrLeu 40

Qy   150 GTAAAACATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60

Qy   210 ATTTCAATAGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAAATGCACA 269
            |||||||||||||||||:::|||||||||||||||||||||||||
Db    61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyGluAsnCysThr 80

Qy   270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnValPheGlnTyrGluAsnTrpAsp 100

Qy   330 CTCTTCATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATAGACATCCCTGACTAT 389
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrProAspTyr 120

Qy   390 GCATCGGTCCGGTCCATTGTAGCATCCTCGACAACATTAGAATTCGACACAGCAGGGATTC 449
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy   450 ACATGGACAGGTGTCACTCACTGAGCCTGCAAAAGGGGATCAGCCGATTC 509
            ||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160

Qy   510 AGCTCAAACCAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 569
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 SerSerAsnGlnGlnThrIleGluLeuTyrIleGlnSerGlyArgValThrValSer 180

Qy   570 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCACATTGAAT 629
            ||||||||||||||||||||||||||||||||||||
Db   181 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 200

Qy   630 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGATTCATCACCCG 689
            ||||||||||||||||||||||||||||||||||||||||||||
Db   201 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 220

Qy   690 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 749
            |||||||||||||||||||||||||||||||||||||:::||||||||
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240
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Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140
            ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   450 ACATGGACAGGTGTCACTCACTGAGCCTGCAAAAGGGGATCAGCCGAT 509

Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCACATTGAAT 569

Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGATTCATCACCCG 629

Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA 689

Db   201 SerSerAsnGlnGlnThrIleGluLeuTyrIleGlnSerGlyArgValThrValSer 220
            |||::||||||||||||||||||||||||||||||||||||||||||||
Qy   690 ACAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT 749

Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly 240
            |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   750 CAATCAGGCAGGATAAGACATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATA 809

Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260
            |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   810 AACAGTAATGCAACTTAGTTGCACCGCGGGGGGATAATTTAAAATGAAAACAGGAAAAGC 869

Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   870 TCTGTAATAGATGACATCAGATGCACCCATAGACATTGTGTCTGAATGTATTACCACAAAT 929

Db   281 SerValMetArgSerAspAlaProIleLeuProGlyAspIleAlaProIleLeuThrProAsn 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   930 GGAAGCCATCCCCAACGACAAAACCATTCAAAATGTGAACAAAGTTACATATGAAAAATGC 989

Db   301 GlySerIleProAsnAspAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   990 CCCAAGTATATCAGGCAAAACACTTAAAGTGCTGGCCACTGGGGATGAGGAATATACCAGA 1049

Db   321 ProLysTyrIleArgGlnAsnThrLeuLysLeuLeuAlaThrGlyMetArgAsnValProGlu 340
            ||||||||||||:||||||||||||||||||||||||||
Qy  1050 AAGCAAATCAGA 1061

Db   341 LysGlnIleArg 344
```

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RESULT 4
Q67103
ID   Q67103      PRELIMINARY;      PRT;   565 AA.
AC   Q67103;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor.
GN   Name=HA1;
OS   Influenza A virus (strain A/equine/Kentucky/1/94).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; unidentified subtype.
OX   NCBI_TaxID=39129;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Equine-2;
RX   MEDLINE=96203953; PubMed=8627254;
RA   Daly J.M., Lai A.C., Binns M.M., Chambers T.M., Barrandeguy M.,
RA   Mumford J.A.;
RT   "Antigenic and genetic evolution of equine H3N8 influenza A viruses.";
RL   J. Gen. Virol. 77:661-671(1996).
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; L39914; AAB36976.1; -.
```

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Pred. No.:             8.94e-148        Length:        344
Score:                 1827.00          Matches:       340
Percent Similarity:    100.00%          Conservative:  4
Best Local Similarity: 98.84%           Mismatches:    0
Query Match:           95.55%           Indels:        0
DB:                    2                Gaps:          0

US-10-826-929A-1 (1-1061) x Q9Q6N5 (1-344)

Qy   30 ATGAAGACAACCATTATTTGATACTACTGACCATTGGGTCTCACAGTCAAAACCCACC   89
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr  20

Qy   90 AGTGGAAACAACAGCCACCATTATGTCTCGGGACACCATGAGTAGCAAATGAACATTG  149
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu  40

Qy  150 GTAAAAACAATAACTGATGACGAAATGAGGTGACAAATGCTACTGAATTAGTTCAGAGC  209
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleIleGluValThrAsnAlaThrGluLeuValGlnSer  60

Qy  210 ATTCAATAGGGAAAAATATGCAACAACTCATATAAAGTCTAGATGGAAGAAATTGCACA  269
         |||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db   61 IleGlnSerIleGlyLysLysCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr  80

Qy  270 TTAATATGATGCAATGCTAGGAGGACACCCCACTGTGATGTCTTCCAGATGAGAATTGGAC  329
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnAsnTyrGluAsnTrpAsp 100

Qy  330 CTCTTCATAGAAGAGCAGGCTTTGCACCCATATGACATCCTGACTAT  389
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  101 LeuPheIleGluArgSerAlaPheSerAsnCysTyrProTyrAspIleProTyr 120

Qy  390 GCATCGTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGAGAGGGATTC  449
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AlaSerLeuArgSerGlyLeuValAlaSerSerGlyThrLeuGluPheLeuAlaGluGlyPhe 140

Qy  450 ACATGACAGGTGTCACTCAAAACGAAGAAGTGGGAGCCTGCAAAAGGGATCAGCCGAT  509
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 ThrTrpThrGlyValThrGlnAsnGluGluValGlyArgGlyLysArgGlySerAlaAsp 160

Qy  510 AGTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGAAACTTCTTACCCCACATTGAAT  569
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGluThrSerTyrProThrLeuAsn 180

Qy  570 GTGACAATGCCTAACATAAAATTTCGACAAACTATACATCTCGGGGGATTCATCACCCG  629
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy  630 AGCTCAAACCAACACCAGCAGAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA  689
         |||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db  201 SerSerAsnGlnAsnLysGlnThrGluLeuTyrIleGlnGluSerGlyArgValThrValSer 220

Qy  690 ACAAAAAGAAGTCAACAAACGATAGTCCCTATATGGGATATGGATGAGAAACAGGGAAAGC  749
         |||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db  221 ThrLysArgSerGlnThrIleValProIleTrpGlySerArgProValArgGly 240

Qy  750 CAATCAGGCAGGATAAGCATATACTGACCATTGTAAAACCTGGAGATATCCTAATGATA  809
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

Qy  810 AACAGTAATGGCAACTTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC  869
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer 280

Qy  870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAATGTATTACACCAAAT  929
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300

Qy  930 GGAAGCATCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC  989
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys 320

Qy  990 CCCAAGTATATCAGGCAAAACACTTTAAAGTCTGGGATGGACCTGGATGAGGAATATACCAGAA 1049
         ||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db  321 ProLysTyrIleArgGlnAsnThrLeuLysSerGlyMetAspLeuAspGluGluTyrArgAsnValProGlu 340

Qy 1050 AAGCAAATCAGA 1061
         ||||||||||||
Db  341 LysGlnIleArg 344
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RESULT 5
Q9Q6N5
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ID   Q9Q6N5          PRELIMINARY;     PRT;   344 AA.
AC   Q9Q6N5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor (Fragment).
GN   Name=HA1;
OS   Influenza A virus (A/equine/Kentucky/1/96(H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=217809;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21395169; PubMed=11504416;
RA   Lai A.C., Chambers T.M., Holland R.E. Jr., Morley P.S., Haines D.M.,
RA   Townsend H.G., Barrandeguy M.;
RT   "Diverged evolution of recent equine-2 influenza (H3N8) viruses in the
RT   Western Hemisphere.";
RL   Arch. Virol. 146:1063-1074(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lai A.C.K.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; AF197248; AAF22352.1; -.
DR   HSSP; P03437; 2VIU.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL        1     15       Potential.
FT   CHAIN        16    >344      hemagglutinin.
SQ   SEQUENCE   344 AA;  38308 MW;  215ED303718BC710 CRC64;
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Alignment Scores:

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Qy    GTAAAACAATAACTGATGACCAAATGAGTGACTGACAAATGCTACTGAATTAGTTCAGAGC   209
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  150
Db    ValLysThrIleThrAspAspAsnGluIleGluValThrAsnAlaThrThrGluLeuGlnSer   60
  41

Qy    ATTTCAATAGGAGAAAATGCAACAACTCATATAAAGTTCTAGATGAGAATTGCACA         269
      ||||||||||||||||||||||||||||||::::|||||||||||||||||
  210
Db    IleSerIleGlyLysIleLysAsnAlaSerTyrArgValLeuAspArgValArgAsnCysThr   80
  61

Qy    TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGCTCTTCCAGTAGTCTTCGAGAATTGGGAC   329
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  270
Db    LeuIleAspAlaMetLeuGlyAspProHisCysAspAlaLeuProValPheGlnTyrAspAspTrpAsp   100
  81

Qy    CTCTTCATAGAAAGAAGCAGCGGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT   389
      |||||||||||||||||||||||||||||:::|||||||||||||||||||||
  330
Db    LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr   120
  101

Qy    GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAGACATTAGAATTCACAGCAGAGGGATTC   449
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  390
Db    AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheHisAlaGluGlyPhe   140
  121

Qy    ACATGGAAGGTGTCACTCAACAAACGGGAGAAGAAGTGCGAGCTGCAAAAGGGATGCCGAT   509
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  450
Db    ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp   160
  141

Qy    AGTTCTTAGCCACTGAATTGGCTAACAAAATCTGGAAACTCTACCCCCATTGAAT         569
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  510
Db    SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn   180
  161

Qy    GTGACAATGCCTACAATAAAAATTCGACAACAATATACATCTGGGGGATTCATCACCCG      629
      |||||||||||||||||||||||||||||||||||||||||||||||||||
  570
Db    ValThrMetProAsnIleLysPheAspAsnLysAsnPheAspLysTyrIleHisTrpGlyIleHisHisPro   200
  181

Qy    AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGATCAGGAGGAGTAACAGTCTCA     689
      ||||||||||:::|||||||||||||||||||||||||||||||||||
  630
Db    SerSerAsnGlnIleGlnThrGluIleGluValArgThrValSer   220

Qy    ACAAAAGAGTCAACAACAGATAGTCCCTAAATATCGGATCTAGACCGTGGGTTAGGGGT     749
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
  690
Db    ThrLysArgSerGlnAsnThrIleIleProAsnIleGlySerArgProValArgGly   240
  221

Qy    CAATCAGGCAGGATAAGCATAACGGACCATTGTAAAACCTGAAGATATCCTAATGATA     809
      |||||||||||||||||||||||||||||||||||||||||||||
  750
Db    GlnSerGlyArgIleSerIleThrTyrArgThrIleValLysProGlyAspIleLeuMetIle   260
  241

Qy    AACAGTAATGCAACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC     869
      ||||||||||||||||||||||||||||||||||||||||||||||
  810
Db    AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuThrGlyLysSer   280
  261

Qy    TCTGTAATGAGATCAGATGCAGTCGCCATAGACATTTGTGTCTGAATGTATTACCACCAAAT     929
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
  870
Db    SerValMetArgSerAspAlaProIleCysIleCysIleThrGluCysThrProAsn   300
  281

Qy    GGAGGCATCCCACGACAAACCATTTCAAAATGAACAAAGTTACATATGGAAAATGC      989
      |||||||||||||||||||||||||||||||||||||||||||||||||
  930
Db    GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys   320

Qy    CCCAAGTATATCAGGCAGCAAAACACTTTAAAGCTGGCCACTGGCGATGAGGAATATACCAGAA  1049
      |||||||||||||||||||||||||||||||::::||||||||||||||||
  990
Db    ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu   340
  321

Qy    AAGCAAATCAGA  1061
      ||||||||||||
  1050
Db    LysGlnIleArg   344
  341
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RESULT 6
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Q9Q6N6
ID   Q9Q6N6;                 PRELIMINARY;    PRT;    344 AA.
AC   Q9Q6N6;
DT   01-MAY-2000  (TrEMBLrel. 13, Created)
DT   01-MAY-2000  (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004  (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor (Fragment).
GN   Name=HA1;
OS   Influenza A virus (A/equine/Kentucky/9/95 (H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=217810;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21395169; PubMed=11504416;
RA   Lai A.C., Chambers T.M., Holland R.E. Jr., Morley P.S., Haines D.M.,
RA   Townsend H.G., Barrandeguy M.;
RT   "Diverged evolution of recent equine-2 influenza (H3N8) viruses in the
RT   Western Hemisphere.";
RL   Arch. Virol. 146:1063-1074 (2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lai A.C.K.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
CC   -!- -
DR   EMBL; AF197247; AAF22351.1; -.
DR   HSSP; P03437; 2VIU.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL        1     15       Potential.
FT   CHAIN        16   >344       hemagglutinin.
FT   NON_TER     344    344
SQ   SEQUENCE   344 AA;  38308 MW;  215ED303718BC710 CRC64;
```

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Alignment Scores:
Pred. No.:                  8.94e-148       Length:         344
Score:                      1827.00         Matches:        340
Percent Similarity:         100.00%         Conservative:     4
Best Local Similarity:      98.84%          Mismatches:       0
Query Match:                95.55%          Indels:           0
DB:                         2               Gaps:             0
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US-10-826-929A-1 (1-1061) x Q9Q6N6 (1-344)
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Qy    ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTTCTCAGTCAAAACCCAACC   89
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  30
Db    MetLysThrThrIleIleLeuLeuLeuThrHisTrpValTyrSerGlnAsnProThr   20
  1

Qy    AGTGGAAACAACACAGCCACATTATGTCTGGGACACCATGCAAATGCAAATGGAACATTG  149
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
  90
Db    SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40
  21
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RESULT 7
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O56857
ID   O56857                  PRELIMINARY;    PRT;    346 AA.
AC   O56857;
DT   01-JUN-1998  (TrEMBLrel. 06, Created)
DT   01-JUN-1998  (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2004  (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin HA1 subunit precursor (Fragment)
OS   Influenza A virus (A/equine 2/Alvdalen/96 (H3N8)).
```

```
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=217820;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Oxburgh L., Akerblom L., Fridberger T., Klingeborn B., Linne T.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oxburgh L.H.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity)
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; Y14059; CAA74387.1; -.
DR   HSSP; P03437; 1E08.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutin_1.
DR   Pfam; PF00509; Hemagglutinin_1.
DR   PRINTS; PR00330; HEMAGGLUTNN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD00225; Hemagglutn_1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL           1     16       Potential.
FT   NON_TER        346    346
SQ   SEQUENCE       346 AA;  38449 MW;  F4755CFF6154C6C9 CRC64;

Alignment Scores:
Pred. No.:                346
Score:                 1822.00
Percent Similarity:     99.71%
Best Local Similarity:  98.55%
Query Match:            95.29%
DB:                        2
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US-10-826-929A-1 (1-1061) x O56857 (1-346)

Qy    30 ATGAAGACAACACCATTATTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCAACC  89
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr  20

Qy    90 AGTGGAACAACACAGCCACATTATGTCTGGGACAACCATGCAAATGGAACATTG 149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu  40

Qy   150 GTAAAACAACATAACTGATGACCAAATTGAGTGACAAATGCTACTGAATTAGTTCAGAGC 209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ValLysThrIleThrAsnAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer  60

Qy   210 AGTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATGCACA 269
         |||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db    61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr  80

Qy   270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC 329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp  100

Qy   330 CTCTTCATAGAAGAGCAGCAGCGCGCTTTCAGCAATTGCTACCCCATATGACATCCCTGACTAT 389
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr  120

Qy   390 GCATCGGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe  140

Qy   450 ACATGACAGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrArgGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp  160
```

Right column:

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Qy   510 AGTTTCTTAGCCGACTGAATTGGCTAACAAAAATCTGGAAAACTCTTACCCCACATTGAAT  569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn  180

Qy   570 GTGACAATGCCTAACAATAAAATTTCGACAACATATACATCTGGGGGATCATCACCCG  629
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysThrTyrIleTrpGlyIleIleHisHisPro  200

Qy   630 AGCTCAAACAACCAGCAGACAGAATTGTACATCCAGAATCAGGACGACGAGTAACAGTCTCA  689
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 SerSerAsnGlnGlnThrGluLeuTyrIleGlnAsnGlnAspAspGluSerGlyArgThrValSer  220

Qy   690 ACAAAAAGAAGTCAACAAACGATAGTCCCTAATATCGGATCAGGATATTTAAATTGAAAACAGGAGAAAGC  749
         ||||||||||||||||||||||||||||||||||||::::||||||||||||||||||||
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProValAlaArgGly  240

Qy   750 CAATCAGGCAGGATAAGCATATACTGACCATTGTAAAACCTGGAGATATCCTAATGATA  809
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle  260

Qy   810 AACAGTAATGCCAACTTAGTTGCACCGGCGGGGATATTTAAATTGAAAACAGGAGAAAGC  869
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer  280

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACATTGTGTGTCTGAATGTATTACACCAAAT  929
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 SerValMetArgSerAspAlaProIleAspIleValCysAlaSerGluCysIleThrProAsn  300

Qy   930 GGAAGCATCCCCAACGACAACAACCATTCAAAATGTGAACAAAGTTACAATGTGAAAATGC  989
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys  320

Qy   990 CCCAAGTATATCAGGCAGAAAACACTTTAAAGCTGCCACTGGCAGAGAATATACCAGAA 1049
         ||||||||||||||||||||||||||||||||||||::::||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu  340

Qy  1050 AAGCAAATCAGA 1061
         ||||||||||||
Db   341 LysGlnIleArg  344
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RESULT 8
O56858
ID   O56858               PRELIMINARY;       PRT;    346 AA.
AC   O56858;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin HA1 subunit precursor (Fragment).
OS   Influenza A virus (A/equi 2/Bolinas/96(H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=217819;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Oxburgh L., Akerblom L., Fridberger T., Klingeborn B., Linne T.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oxburgh L.H.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity)
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; Y14060; CAA74388.1; -.
DR   HSSP; P03437; 1E08.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutin_1.
```

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DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTNIN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn_1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL      1     16       Potential.
FT   NON_TER     1    346
SQ   SEQUENCE  346 AA;  38449 MW;  F4755CFF6154C6C9 CRC64;

Alignment Scores:
Pred. NO.:  PF00509; Hemagglutinin; 1.
Score:                     1822.00
Percent Similarity:          99.71%
Best Local Similarity:       98.55%
Query Match:                 95.29%
DB:

Length:         346
Matches:        339
Conservative:     4
Mismatches:       1
Indels:           0
Gaps:             0
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US-10-826-929A-1 (1-1061) x O56858 (1-346)

```
Qy       30 ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC  89
Db        1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy       90 AGTTGGAAACAACAGCACAGCCACATTATGTCTGGGACACCAGCAGTGCAAATGCAACATTG 149
Db       21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy      150 GTAAAAACAATAACATGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
Db       41 ValLysThrIleThrAsnAspGlnIleGluGluValThrAlaThrGluLeuValGlnSer   60

Qy      210 ATTTCAATAGGGAAAAATATGCAACAACTCATATAAGTTCTAGATGGAAGAAATTGCACA 269
Db       61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr   80

Qy      270 TTAATAGATGCAATGCTAGGAGACACCCCCCCCACTGTGATGCTTCCAGTGAGAATTGGGAC 329
Db       81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnAsnTyrGluAsnTrpAsp 100

Qy      330 CTCTTCATAGAAGAAGAGCAGCGCTTCAGCAATTGCATACCCATATGACATCCCTGACTAT 389
Db      101 LeuPheIleGluGluAspGlnAlaPheSerAsnCysTyrProTyrAspIleProAspTyr  120

Qy      390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAAATTCACAGCAGAGGGATTC 449
Db      121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe  140

Qy      450 ACATGGACAGGTGTCACTCAAAACGGAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGGAT 509
Db      141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp  160

Qy      510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTGAAT 569
Db      161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerTyrProThrLeuAsn  180

Qy      570 GTGACAATGCCTAACAATAAAAATTCGACAAACTATACATCTGGGGATTCATCACCCG 629
Db      181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro  200

Qy      630 AGCTCAAACCAACAGCAGACAGATTGTACATCCAAGAATCAGAGCGAGTAACAGTCTCA 689
Db      201 SerSerAsnGlnGlnGlnThrGluLeuTyrIleGlnGluSerGlyArgValThrValSer  220

Qy      690 ACAAAAGAGTCAACAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT 749
Db      221 ThrLysGlnSerGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly  240

Qy      750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGAAACCTGAGAGATATCCTAATGATA 809
Db      241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle  260

Qy      810 AACAGTAATGGCAACTAGTTGCACCGCGGGGGGATATTTTAAATTGAAAACAGGGAAAAGC 869
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```
Db      261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLeuLysLysThrGlyLysSer  280

Qy      870 TCTGTAATGAGATCAGATGCAGACACCATTGCTGTGTCTGATGTATTACACCCAAAT  929
Db      281 SerValMetArgSerAspAlaProIleAlaValSerAspValLeuHisHisProAsn  300

Qy      930 GGAAGCATCCCCAACGACAACAAACCATTCAAAATGTGAACAAGTTACATATGGAAAATGC  989
Db      301 GlySerIleProAsnAspAsnLysProPheLysMetValAsnLysValThrTyrGlyLysCys 320

Qy      990 CCCAAGTATATCAGGCAAAACACTTAAAGCTGGATGAGGAATATACCAGAA 1049
Db      321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340

Qy     1050 AAGCAAATCAGA 1061
Db      341 LysGlnIleArg  344
```

RESULT 9

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ID   Q67105               PRELIMINARY;      PRT;   565 AA.
AC   Q67105;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor.
GN   Name=HA1;
OS   Influenza A virus (strain A/equine/Florida/1/93).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; unidentified subtype.
OX   NCBI_TaxID=39124;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Equine-2;
RX   MEDLINE=96203953;  PubMed=8627254;
RA   Daly J.M., Lai A.C., Binns M.M., Chambers T.M., Barrandeguy M.,
RA   Mumford J.A.;
RT   "Antigenic and genetic evolution of equine H3N8 influenza A viruses.";
RL   J. Gen. Virol. 77:661-671(1996).
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; L39916; AAB36978.1; -.
DR   HSSP; P03437; 1QU1.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTNIN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn_1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL      1     15       Potential.
FT   CHAIN      16    344       hemagglutinin.
FT   CHAIN      16    565       hemagglutinin.
SQ   SEQUENCE  565 AA;  63734 MW;  740D31FB86D6AAD1 CRC64;

Alignment Scores:
Pred. No.:             8.34e-147
Score:                   1816.00
Percent Similarity:       99.71%
Best Local Similarity:    98.26%
Query Match:              94.98%
DB:

Length:          565
Matches:         338
Conservative:      5
Mismatches:        1
Indels:            0
Gaps:              0
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US-10-826-929A-1 (1-1061) x Q67105 (1-565)

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Qy       30 ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTCACAGTCAAAACCCAACC  89
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AC   Q9YJV1;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor (Fragment)
OS   Influenza A virus (A/equine/LaPlata/1/93 (H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=225098;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H3N8;
RA   Lindstrom S.E., Endo A., Pecoraro M.R., Sugita S., Damiani A.,
RA   Hiromoto Y., Kanata M., Kumanomido T., Nerome K.;
RL   Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; D30686; BAA33947.1; -.
DR   HSSP; P03442; 1IBN.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutnin_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL      1     16      Potential.
FT   CHAIN      17    343      hemagglutinin 1 (HA1).
FT   NON_TER   362    362
SQ   SEQUENCE  362 AA;  40158 MW;  71C864B0C2DD4F6B CRC64;

Alignment Scores:
Pred. No.:                               Length:            362
Score:                 1.42e-146         Matches:           337
Percent Similarity:       99.42%         Conservative:        5
Best Local Similarity:    97.97%         Mismatches:          2
Query Match:              94.82%         Indels:              0
DB:                            2         Gaps:                0


US-10-826-929A-1 (1-1061) x Q9YJV1 (1-362)

Qy    30 ATGAAGACAACCATTATTTGATACTACTGACCATTGGGTCTACAGTCAAAACCCAACC    89
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetLysThrThrIleIleLeuIleLeuIleLeuThrHisTrpValTyrSerGlnAsnProThr  20

Qy    90 AGTGGAAACAACACAGCCACATTATGTCTCGGACACCACCATTATGAACATTG   149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu   40

Qy   150 GTAAAAACAATAACTGATGACCAAAATGCTACTCATATAAAGTTCTAGATGGAAGAAATTGCACA   209
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ValLysThrIleThrAspAspGlnAsnAlaThrHisIleLysPheLeuAspGlyArgGlnLeuValLeuValGlnSer   60

Qy   210 ATTCAATAGGAAAATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATTGCACA   269
         |||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db    61 IleSerGluIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr   80

Qy   270 TTAATAGATGCAATGTTAGGAGACCCCCACTGTGATGTCTTCCAGAATGAGACATTGGGAC   329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnAsnGluThrTrpAsp  100

Qy   330 CTCTTCATAGAAAGAAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT   389
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr  120

Qy   390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC   449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe  140

Qy   450 ACATGACAGTGTCACTCAAAACGGAAGAAGTGGAGCCGTGCAAAAGGGGATCAGCCGAT   509
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp  160

Qy   510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCACATTGAAT   569
         ||:|||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProTyrLeuAsn  180

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAAATATACATCTGGGGATTCATCACCCG   629
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysTyrIlePheLeuTrpGlyIleHisHisPro  200

Qy   630 AGCTCAAACCACACAGACGAGAATTGTACATCCAAGAATCAGAGCGAGTAACAGTCTCA   689
         ||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db   201 SerSerAsnGlnGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer  220

Qy   690 ACAAAAAGAGAGTCAACAAAACCGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT   749
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly  240

Qy   750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATA   809
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle  260

Qy   810 AACACAGTAATGCAACTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGC   869
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer  280

Qy   870 TCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTCTGAAATGTATTACACCAAAT   929
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 SerValMetArgSerAspAlaProIleAspThrCysIleSerGluCysIleThrProAsn  300

Qy   930 GGAAGCATCCCAAGCACAGACAAAACCATTCAAAATGTGAACAAAGTTACACATATGGAAAATGC   989
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GlySerIleSerAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys  320

Qy   990 CCCAAGTATATATCAGGCAAAACACTTAAAGCTGGCCACTGGGCAATATACCAGAGA  1049
         ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu  340

Qy  1050 AAGCAAATCAGA  1061
         ||||||||||||
Db   341 LysGlnIleArg  344


RESULT 10
Q9YJV1
ID   Q9YJV1     PRELIMINARY;      PRT;     362 AA.
```

```
DR   HSSP; P03437; 1QU1.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid hemag.
DR   InterPro; IPR001364; Hemagglutn_.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL      1     15       Potential.
FT   CHAIN      16    344       hemagglutinin.
FT   CHAIN      16    565       hemagglutinin.
SQ   SEQUENCE   565 AA;  63714 MW;  13135C9B04CC560D CRC64;
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Alignment Scores:

```
Pred. No.:                                Length:         565
Score:                    1813.00         Matches:        337
Percent Similarity:       99.42%          Conservative:     5
Best Local Similarity:    97.97%          Mismatches:       2
Query Match:              94.82%          Indels:           0
DB:                                2      Gaps:             0
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US-10-826-929A-1 (1-1061) x Q67102 (1-565)

```
Qy     30 ATGAAGACAACCATTATTTGATACTACTGGGTCTACAGTCAAAACCCAACC   89
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr   20

Qy     90 AGTGAAACAACACAGCCACCATTATGTCTGGGACACCATTGCAATGGAACATTG  149
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAlaAsnGlyThrLeu   40

Qy    150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC  209
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 ValLysThrIleThrAspAspGlnIleGluGluValThrAsnAlaThrGluLeuValGlnSer   60

Qy    210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAGAAAATTGCACA  269
          ||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr   80

Qy    270 TTAATAGATGCAATGCTAGAGACCCCCACTGTGATGTCTTCCAGTATGAGAATTGGGAC  329
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 LeuIleAspAlaMetLeuGluThrProThrValMetSerSerSerMetArgIleGlyAsp   100

Qy    330 CTCTTCATAGAAAAGAAGCAGCGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT  389
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 LeuPheIleGluLysSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr   120

Qy    390 GCATCGCTCCGGTCCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC  449
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AlaSerLeuArgSerHisCysSerIleLeuArgThrLeuGluPheThrAlaGluGlyPhe   140

Qy    450 ACATGGACAGGTGTCACTCAAAACCGGAAGAGTGGAGCCTGCAAAAAGGGGGATCAGCCGAT  509
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 ThrTrpThrGlyValThrGlnAsnArgLysSerGlyAlaCysLysLysGlySerAlaAsp   160

Qy    510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAAATCTTACCCCACATTGAAT  569
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 SerPhePheSerArgLeuAsnTrpLeuThrLysIleLeuProHisIleAsn   180

Qy    570 GTGACAATGCCTAACAACAATAAAAAATTCGACAAACTATACATCTCGGGGATTCATCACCCG  629
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ValThrMetProAsnAsnAsnLysLysPheAspLysLeuTyrIleHisHisPro   200

Qy    630 AGTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCA  689
          ||||||||      |||||::||||||||||||||||||||||||
Db    201 SerSerAsnAsnGluGlnThrLysGluGlnThrLysLeuTyrIleGluGlySerGlyValThrValSer   220

Qy    690 ACAAAAGAAGTCAACAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGGT  749
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProTrpValArgGly   240
```

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Query Match:       94.82%        Indels:    0
DB:                2             Gaps:      0

US-10-826-929A-1 (1-1061) x Q67107 (1-565)

Qy     30 ATGAAGACAACCATTATTTGATACTACTGACCAGTCAATGGGTCTCACAGTCAAAACCCACC   89
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetLysThrThrIleLeuIleLeuLeuLeuThrHisTrpValTyrSerGlnAsnProThr    20

Qy     90 AGTGGAAACAACACAGCCACCATTATGTCTGGACACCATGTCGGACAATGGCAAATGGAACATTG  149
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 SerGlyAsnAsnThrAlaThrIleLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu    40

Qy    150 GTAAAAACAATAACTGATGACCAAAATGAGGTGACAAATGTACTACTGAATTAGTTCAGAGC   209
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 ValLysThrIleThrAspAspGlnAsnGluValThrAsnAlaThrGluLeuValGlnSer    60

Qy    210 ATTTCAATAGGAGAAAATATGCAACAACTCATATAAAGTTCTAGATGAAGAGAAATTGCACA   269
          |||||||||||||||||||||||||||||||||||||||::|||||||||||||||||||
Db     61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr    80

Qy    270 TTAATAGATGCAATGCTAGGAGCAGCCCCACTGTGAGTGTCTTCCAGTATGAGAATTGGGAC   329
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp   100

Qy    330 CTCTTCATAGAAGAGAGCAGCGCTTTCAGCAATTGCTACCCATATGACATCCCTGACTAT   389
          |||||||||||||||||||||||||||||||||||||||||||||||||||::|||||
Db    101 LeuPheIleGluArgSerSerAlaPheSerSerCysTyrProTyrAspIleProAspTyr   120

Qy    390 GCATCGTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC   449
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe   140

Qy    450 ACATGGACAGGTGTCACTCAAAACGGGAGAAGTGGAGCTCGAAAAGGGATCAGCCGAT   509
          |||||||||||||||||||||||||||||::||||||||||||||||||||||||||
Db    141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlySerCysLysGlySerAlaAsp   160

Qy    510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTGAAT   569
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn   180

Qy    570 GTGACAATGCCTAACATAAATAAAATTCGACAAACTATACATCTGGGGGATTCATCACCCG   629
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ValThrMetProAsnAsnLysAsnLysIleArgGlnThrIleHisLeuGlyGlyIleHisPro   200

Qy    630 AGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAGCAGAGTAACAGTCTCA   689
          |||||||||||||||||::|||||||||||:||||||||||||||||||||||||||||
Db    201 SerSerAsnGluGlnGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer   220

Qy    690 ACAAAAGAAGTCAACAACGATAGTCCCTATATCGGATCTTAGACCGTGGGTTAGGGGT   749
          |||||||||||||||||||::||||||||||||||||||||||||||||||||||||
Db    221 ThrLysGluGlnGlnThrIleIleProAsnIleGlySerArgProValArgGly   240

Qy    750 CAATCAGGCAGGATAAGCCATATACTGACCATTGTAAAACCTGGAGATATCCTAATGATA   809
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle   260

Qy    810 AACAGTAATGGCAACTAGTTGCACCGCGGGATATTTAAATTGAAAACAGGGAAAAGC   869
          ||||||||||||||||||||||||||||||||||||||::|||||||||||||||
Db    261 AsnSerAsnGlyAsnLeuValAlaProLeuGlyTyrTyrPheLysLysThrGlyLysSer   280

Qy    870 TCTGTAATGAGATCAGATGCACCCCATAGACATTTGTGTCTCGAATGTATTACACCAAAT   929
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn   300

Qy    930 GGAAGCATCCCAACGACAAACCATTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA  1049
          |||||||||||||||||||||||||||||||||::|||||||||||||::|||||||
Db    301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys   320

Qy   1050 AAGCAAATCAGA  1061
          ||||||||||||
Db    341 LysGlnIleArg   344
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RESULT 12
Q67107

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ID   Q67107        PRELIMINARY;      PRT;   565 AA.
AC   Q67107;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor.
GN   Name=HA1;
OS   Influenza A virus (strain A/equine/Kentucky/1/91).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; unidentified subtype.
OX   NCBI_TaxID=38828;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Equine-2;
RX   MEDLINE=96203953; PubMed=8627254;
RA   Daly J.M., Lai A.C., Binns M.M., Chambers T.M., Barrandeguy M.,
RA   Mumford J.A.;
RT   "Antigenic and genetic evolution of equine H3N8 influenza A viruses.";
RL   J. Gen. Virol. 77:661-671(1996).
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity)
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; L39918; AAB36980.1; -.
DR   HSSP; P03437; 1QU1.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL        1     15       Potential.
FT   CHAIN        16    344       hemagglutinin.
FT   CHAIN        16    565       hemagglutinin.
SQ   SEQUENCE   565 AA;  63704 MW;  18B320F59B57D93A CRC64;
```

Alignment Scores:
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Pred. No.:             1.51e-146     Length:          565
Score:                 1813.00       Matches:         336
Percent Similarity:    100.00%       Conservative:    8
Best Local Similarity: 97.67%        Mismatches:      0
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Qy   210 ATTTCAATAGGAGAAATATGCAACACTCATATAAAGTTCTAGATGGAAGAAATTGCACA 269
         ||||||||||||||||||||||||||:::||||||||||||||||||||||
Db    61 IleSerIleGlyIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr    80

Qy   270 TTAATAGATGCAATGCTAGGAGACCCCACTGTGATGTCTTCCAGTATGAGAATTGGAC 329
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnPheArgIleTrpAspAsp 100

Qy   330 CTCTTCATAGAAAGAGCAGCGCCTTCAGCAATTGCTACCCATATGACATCCCTGACTAT 389
         |||||||||||||||||||||||||||||||||||||||||||||
Db   101 LeuPheIleGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy   390 GCATCGTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC 449
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe 140

Qy   450 ACATGGACAGGTGTCACTCAAACGGAAGAAGTGGAGCCTGCAAAAGGGGATCAGCCGAT 509
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ThrTrpThrGlyValThrGlnThrGluGluValGluProAlaLysGlyAspGlnProAsp 160

Qy   510 AGTTTCTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACATTGAAT 569
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   161 SerPhePheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn 180

Qy   570 GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGGATTCATCACCG 629
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyIleHisHisPro 200

Qy   630 AGCTCAAACCAACAGCAGCAGATTGTACATCCAAGAATCAGGAGGACGAGTAACAGTCTCA 689
         ||||||||||||||||:::||||||||||||||||||||||||||
Db   201 SerSerAsnGlnGlnIleValHisLeuTyrIleGlnGluSerGlyValThrValSer 220

Qy   690 ACAAAAAGAGTCAACAACGATAGTCCCTAATATCGGATCAGTAGTAGCCGGTCGTGGGT 749
         ||||||||||||||||:::||||||||||||||||||||||||
Db   221 ThrLysArgSerGlnGlnThrIleIleProAsnIleGlySerArgProValArgGly 240

Qy   750 CAATCAGGCAGGATAAGCATAAGCATATACTGGACCATTGTAAAACTGGAGATATCCTAATGATA 809
         ||||||||||||||||||||||||||||||||||||||||||||
Db   241 GlnSerGlyArgIleSerIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle 260

Qy   810 AACAGTAATGGCAACTAGTTGCACCGCCGGGGATATTTTAAATTGAAACAGGGAAAAGC 869
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuArgThrGlyLysSer 280

Qy   870 TCTGTAATGAGATCAGATGCAGCACCCATAGACATTGTGTGTCTGAATGTATTACCCAAAT 929
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   281 SerValMetArgSerAspAlaProIleAspIleCysValSerGluCysIleThrProAsn 300

Qy   930 GGAAGCATCCCAACGACAAACATTCAAAATGCAACAAGTTACATATGAAAATGC 989
         |||||||||||||||||||||||||||||||||||::||||||||||
Db   301 GlySerIleSerArgAsnAspProPheGlnIleAsnValAsnLysValThrTyrGlyLysCys 320

Qy   990 CCCAAGTATATCAGGAAACACTTAAAGCTGGGATGAGGAATATACCAGAA 1049
         |||||||||||||||||||||||||||||||::||||||||||||||
Db   321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnValProGlu 340

Qy  1050 AAGCAAATCAGA 1061
         ||||||||||||
Db   341 LysGlnIleArg 344
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RESULT 14
Q67106
ID   Q67106   PRELIMINARY;   PRT;   565 AA.
AC   Q67106;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor.
GN   Name=HA1;
OS   Influenza A virus (A/equine/Kentucky/1/92(H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=225095;

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Qy  1050 AAGCAAATCAGA 1061
         ||||||||||||
Db   341 LysGlnIleArg 344
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RESULT 13
Q9Q6P1
ID   Q9Q6P1   PRELIMINARY;   PRT;   344 AA.
AC   Q9Q6P1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor (Fragment).
GN   Name=HA1;
OS   Influenza A virus (A/equine/Florida/1/94(H3N8)).
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=217815;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21395169; PubMed=11504416;
RA   Lai A.C., Chambers T.M., Holland R.E. Jr., Morley P.S., Haines D.M.,
RA   Townsend H.G., Barrandeguy M.;
RT   "Diverged evolution of recent equine-2 influenza (H3N8) viruses in the
RT   Western Hemisphere.";
RL   Arch. Virol. 146:1063-1074(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lai A.C.K.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC   cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC   (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; AF197242; AAF22346.1; -.
DR   HSSP; P03437; 2VIU.
DR   GO; GO:0019903; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutin.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL   1   15   Potential.
FT   CHAIN   16   >344   hemagglutinin.
FT   NON_TER   344
SQ   SEQUENCE   344 AA; 38270 MW; 2A387D226D45880D CRC64;

Alignment Scores:
Pred. No.:   Length: 344
Score: 1.72e-146   Matches: 337
                       1812.00   Conservative: 5
Percent Similarity: 99.42%   Mismatches: 2
Best Local Similarity: 97.97%   Indels: 0
Query Match: 94.77%   Gaps: 0
DB: 2

US-10-826-929A-1 (1-1061) x Q9Q6P1 (1-344)

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Qy   30 ATGAAGACAACAACCATATTTGATACTACTGACCCATTGGTCTACAGTCAAAACCCAACC 89
         |||||||||||||||||||||||||||||
Db    1 MetLysThrThrIleLeuIleLeuIleLeuLeuThrHisTrpAlaTyrSerGlnAsnProThr 20

Qy   90 AGTGGAAACAACACAGCCACCACCATTATGTCTGGGACACCACCATGCAGTAGCAAATTG 149
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrThrIleCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu 40

Qy  150 GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC 209
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer 60
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```
Db  161 SerPheSerArgLeuAsnTrpLeuThrLysSerGlyAsnSerTyrProThrLeuAsn        180
Qy  570 GTGACAATGCCTAACATAACATAAAAATTTCGACAACATATACATCTGGGGATTCATCACCCG  629
        ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||||
Db  181 ValThrMetProAsnAsnLysAsnPheAspLysTyrIleTrpGlyIleTrpIleHisPro     200

Qy  630 AGCTCAAACCAACAGCAGACGAATTGTACATCCAGAATCCAGAGCAGAGTAACAGTCTCA     689
        |||||||   :::||||||||||||||||||||||||||||||||||||||||||||||||
Db  201 SerSerAsnAsnGluGlnThrLysLeuTyrIleGlnGluThrGlyArgValThrValSer     220

Qy  690 ACAAAAGAAGTCAACAAACGATAGTCCCTATATCGGATTCAGAATGTATTACACCAAAT     749
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  221 ThrLysArgSerGlnGlnThrIleLeuProAsnIleGlySerArgProValArgGly      240

Qy  750 CAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATA    809
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGlyAspIleLeuMetIle    260

Qy  810 AACAGTAATGGCAACTTAGTTGCACCCGGGGATATTTAAATTGAAAACAGGGAAAAGC     869
        ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db  261 AsnSerAsnGlyAsnLeuValAlaProGlyAspIleTyrPheLysLeuArgThrGlyArgSer 280

Qy  870 TCTGTAATGAGATCAGATGACCCCATAGACATTTGTGTGTCTGAATGTATTACACCAAAT    929
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 SerValMetArgSerAspAspProIleAspIleCysValSerGluCysIleThrProAsn    300

Qy  930 GGAAGCATCCCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACTACATGGAAAATGC   989
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrThrTyrGlyLysLysCys 320

Qy  990 CCCAAGTATATCAGGCAAAACACTTTAAAGCTGGCCACTGGGATGAGGAATATACCAGAA  1049
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyLeuAlaThrGlyMetArgAsnValProGlu 340

Qy 1050 AAGCAAATCAGA   1061
        ||||||||||||
Db  341 LysGlnIleArg   344
```

RESULT 15

Q9Q6N8

```
ID   Q9Q6N8       PRELIMINARY;      PRT;    344 AA.
AC   Q9Q6N8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemagglutinin precursor (Fragment)
GN   Name=HA1;
OS   Influenza A virus (A/equine/Argentina/2/94(H3N8))
OC   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC   Influenzavirus A; H3N8 subtype.
OX   NCBI_TaxID=217812;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21395169; PubMed=11504416;
RA   Lai A.C., Chambers T.M., Holland R.E. Jr., Morley P.S., Haines D.M.,
RA   Townsend H.G., Barrandeguy M.;
RT   "Diverged evolution of recent equine-2 influenza (H3N8) viruses in the
RT   Western Hemisphere.";
RL   Arch. Virol. 146:1063-1074(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lai A.C.K.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; AF197245; AAF22349.1; -.
DR   HSSP; P03437; 2VIU.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Equine-2;
RX   MEDLINE=96203953; PubMed=8627254;
RA   Daly J.M., Lai A.C., Binns M.M., Chambers T.M., Barrandeguy M.,
RA   Mumford J.A.;
RT   "Antigenic and genetic evolution of equine H3N8 influenza A viruses.";
RL   J. Gen. Virol. 77:661-671(1996).
CC   -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
CC       cell receptors and for initiating infection (By similarity).
CC   -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
CC       (HA1 and HA2) linked by a disulfide bond (By similarity).
CC   -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR   EMBL; L39917; AAB36979.1; -.
DR   HSSP; P03437; 1QU1.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR008980; Capsid_hemag.
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutn_1.
DR   Pfam; PF00509; Hemagglutinin; 1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD00225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL        1     15       Potential.
FT   CHAIN        16    344       hemagglutinin.
FT   CHAIN        16    565       hemagglutinin.
SQ   SEQUENCE   565 AA;   63770 MW;   8459CC658EADC80F CRC64;
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Alignment Scores:
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Pred. No.:
Score:                   1810.00
Percent Similarity:      99.71%
Best Local Similarity:   97.38%
Query Match:             94.67%
DB:
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Length:        565
Matches:       335
Conservative:    8
Mismatches:      1
Indels:          0
Gaps:            2
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US-10-826-929A-1 (1-1061) x Q67106 (1-565)

```
Qy   30 ATGAAGACAACAACCATTATTTGATACTACTGGATCCTACAGTCAAAACCCAACC        89
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MetLysThrThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr  20

Qy   90 AGTGAAAACAACACAGCCACCATTATGTCTGGACACCATGCAGTAGCACAATGCAAATGGAACATTG 149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAlaAsnGlyThrLeu    40

Qy  150 GTAAAACAATAACTAACTACAACTGAGGTGAACAAATGAGTGACCTACTAGTTCAGAGC      209
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer      60

Qy  210 ATTTCAATAGGGAAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAATGCACA     269
         |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||
Db   61 IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspGlyArgAsnCysThr      80

Qy  270 TTAATAGATGCAATGCTAGGAGACCCCCACTGTCATGTCTTCCAGTATGAGAATTGGGAC    329
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGluAsnTrpAsp    100

Qy  330 CTCTTCATAGAAGAAGCAGCAGCGCTTCAGCAATTGCTACCATATGACATCCCTGACTAT   389
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 LeuPheIleGluGluArgSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr 120

Qy  390 GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACATTAGAATTCACAGCAGAGGGATTC   449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AlaSerLeuArgSerIleValAlaSerSerGlyThrLeuGluPheThrAlaGluGlyPhe    140

Qy  450 ACATGGACAGGTGTCACTCAAAACGGAAGAAGTGGAGCCTGCAAAAGGGATCAGCCGAT   509
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141 ThrTrpThrGlyValThrGlnAsnGlyArgSerGlyAlaCysLysArgGlySerAlaAsp    160

Qy  510 AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTGGAAACTCTTACCCCACCATTGAAT 569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
DR   InterPro; IPR001364; Hemagglutn.
DR   InterPro; IPR000149; Hemagglutinin_1.
DR   Pfam; PF00509; Hemagglutinin_1.
DR   PRINTS; PR00330; HEMAGGLUTN1.
DR   PRINTS; PR00329; HEMAGGLUTN12.
DR   ProDom; PD000225; Hemagglutn; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Signal.
FT   SIGNAL     1      15      Potential.
FT   CHAIN     16    >344      hemagglutinin.
FT   NON_TER  344     344
SQ   SEQUENCE 344 AA; 38366 MW; 68F1B5AABE8DBFFF CRC64;

Alignment Scores:
Pred. No.:              3.79e-146        Length:         344
Score:                  1808.00          Matches:        337
Percent Similarity:     99.42%           Conservative:   5
Best Local Similarity:  97.97%           Mismatches:     2
Query Match:            94.56%           Indels:         0
DB:                                      Gaps:           0
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US-10-826-929A-1 (1-1061) x Q9Q6N8 (1-344)

```
Qy    30  ATGAAGACAACCATTATTTTGATACTACTGACCCATTGGGTCTACAGTCAAAACCCACC         89
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Db     1  MetLysThrThrIleIleLeuIleLeuLeuThrHisTrpValTyrSerGlnAsnProThr         20

Qy    90  AGTGGAAACAACACAGCCACATTATGTCTGGGACACCAGTAGCAGAAATGGAACATTG        149
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21  SerGlyAsnAsnThrAlaThrLeuCysLeuGlyHisHisAlaValAlaAsnGlyThrLeu        40

Qy   150  GTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGC      209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41  ValLysThrIleThrAspAspGlnIleGluValThrAsnAlaThrGluLeuValGlnSer       60

Qy   210  ATTTCAATAGGGAAAAATATGCAACAACTCATATAAAGTCTAGATGGAAGAAATTGCACA      269
          |||||||||||||||||||||||||   :::|||||||||||||||||||||||||
Db    61  IleSerIleGlyLysIleCysAsnAsnSerTyrArgValLeuAspAspValLysArgAsnCysThr   80

Qy   270  TTAATAGATGCAATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATGGAATTGGGAC      329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81  LeuIleAspAlaMetLeuGlyAspProHisCysAspValPheGlnTyrGlyIleTrpAsp      100

Qy   330  CTCTTCATAGAAGAGAGCAGCGCTTTCAGCAATGCTACCCATAATGACATCCCTGACTAT      389
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101  LeuPheIleGluGluSerSerAlaPheSerAsnCysTyrProTyrAspIleProAspTyr      120

Qy   390  GCATCGCTCCGGTCCATTGTAGCATCCTCAGGAACCATTAGAATTCACAGCAGAGGGATTC    449
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AlaSerLeuArgSerIleValAlaSerSerGlyThrIleArgIleHisSerArgGlyPhe      140

Qy   450  ACATGGCAGGTGTCACTCAAAACGGAGAAGTGGAGCCTGCAAAAGGGGATCAGCAGCGAT    509
          ||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db   141  ThrTrpGlnValThrGlySerLeuLysThrGluLysTrpSerLeuGlnLysGlySerAlaAsp   160

Qy   510  AGTTTCTTTAGCCGACTGAATTGGCTAACAAAATCTTACCCCACATTGAAT          569
          :::|||||||||||||||||||||||||||||||||||||||||||||||
Db   161  SerPhePheSerArgLeuAsnTrpLeuThrLysSerTyrProThrLeuAsn          180

Qy   570  GTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGATTCATCACCCG    629
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ValThrMetProAsnAsnLysAsnPheAspLysLeuTyrIleTrpGlyPheIleGlyHisHisPro  200

Qy   630  AGCTCAAACCAACAGCAGACAGATTGTACATCCAAGAATCAGGAGCGAGTAACAGTCTCA    689
          |||||||  :::||||||||||||||||||||||||||||||||||||||||||||
Db   201  SerSerAsnAsnGluGlnThrLysLeuTyrIleGlnGluSerGlyArgValThrValSer     220

Qy   690  ACAAAAGAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGTTAGGGGT     749
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221  ThrLysSerGlnGlnThrIleSerProAsnIleGlySerArgProTrpValArgGly      240

Qy   750  CAATCAGGCAGGATAAAGCATATACTGGACCATTGTAAAACCTGAAGATCCTAATGATA    809
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GlnSerGlyArgIleSerIleTyrTrpThrIleValLysProGluAspProAsnIleLeuMetIle  260

Qy   810  AACAGTAATGGCAACTTAGTTGCACCGCCGGGGATATTTAAATTGAAACAGGGAAAAGC    869
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261  AsnSerAsnGlyAsnLeuValAlaProArgGlyTyrPheLysLeuLysThrGlyLysSer     280

Qy   870  TCTGTAATGAGATCAGATGCACCCATAGACATTGTGTCTGAATGTATTACCACCAAAT    929
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281  SerValMetArgSerAspAlaProIleAspIleValSerGluCysIleThrProAsn       300

Qy   930  GGAAGCATCCCAACGACAAACCATTCAAAATGTGAACAAAGTTACATATGGAAAATGC    989
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GlySerIleProAsnAspLysProPheGlnAsnValAsnLysValThrTyrGlyLysCys     320

Qy   990  CCCAAGTATATCAGGCAAAACACTTAAAGCTGCCACTGGGATGGAGAATATACCAGAA   1049
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321  ProLysTyrIleArgGlnAsnThrLeuLysLeuAlaThrGlyMetArgAsnIleProGlu     340

Qy  1050  AAGCAAATCAGA   1061
          ||||||||||||
Db   341  LysGlnIleArg   344
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Search completed: February 27, 2005, 18:32:06
Job time : 227 secs

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    March  1, 2005, 03:15:42 ; Search time 4077 Seconds
                                       (without alignments)
                                       9905.860 Million cell updates/sec

Title:     US-10-826-929A-1
Perfect score: 1061
Sequence:  1 agcaaaagcagggatcatt........taccagaaagcaaatcaga 1061

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:  3429544 seqs, 1903213400 residues

Total number of hits satisfying chosen parameters:  68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  EST:*
            1: gb_est1:*
            2: gb_est2:*
            3: gb_htc:*
            4: gb_est3:*
            5: gb_est4:*
            6: gb_est5:*
            7: gb_est6:*
            8: gb_gss1:*
            9: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

c	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	44.6	4.2	878	9	CNS0187R	AL108993 Drosophil
	2	43.9	4.3	598	8	AQ636729	AQ636729 RPCI-11-4
c	3	43.8	4.1	820	8	CC081372	CC081372 CSU-K33r.
c	4	42.8	4.0	854	9	CNS0090S	AL052980 Drosophil
	5	42.4	4.0	1101	9	CNS0106X	AL098595 Drosophil
	6	42	4.0	665	6	BY725844	BY725844 Drosophil
c	7	41.6	3.9	1106	9	CNS001RE	AL078654 Drosophil
c	8	41.4	3.9	733	8	AQ055729	AQ055729 CIT-HSP-2
	9	41	3.9	1101	9	CNS00H6Y	AL073010 Drosophil
c	10	41	3.9	1362	9	AG429915	AG429915 Mus muscu
c	11	40.8	3.9	879	5	BX693295	BX693295
c	12	40.8	3.8	1342	9	CL650318	CL650318 CH213-288
	13	40.6	3.8	503	8	BH744818	BH744818 gt42d05.b
c	14	40.6	3.8	643	7	CK563538	CK563538 rswpb0 00
	15	40.6	3.8	968	3	CNS0172G	AL107506 Drosophil
	16	40.4	3.8	610	8	AZ345336	AZ345336 1M0079P14
c	17	40.4	3.8	1005	9	AL067043	AL067043 Drosophil
c	18	40.2	3.8	470	7	CK747765	CK747765 nad03-4cs
c	19	39.8	3.8	1101	9	CNS00LT2	AL078714 Drosophil
c	20	39.8	3.8	1400	9	AG430154	AG430154 Mus muscu
	21	39.6	3.7	1011	3	CNS08VXN	BX030807 single re
	22	39.4	3.7	498	8	AZ026564	AZ026564 RPCI-23-3
	23	39.4	3.7	558	8	AZ400010	AZ400010 1M0166B12
	24	39.4	3.7	687	5	BQ476807	BQ476807 meladema2
c	25	39.4	3.7	720	9	CW016552	CW016552 ZMMBLc000
c	26	39.2	3.7	580	1	AV913773	AV913773 AV913773
c	27	39.2	3.7	830	9	CNS06P7Z	AL409029 T7 end of
c	28	39.2	3.7	1006	9	CL484743	CL484743 SAIL_401
c	29	39	3.7	589	8	AQ992610	AQ992610 RPCI-23-3
c	30	39	3.7	641	8	AZ880556	AZ880556 RPCI-23-1
	31	39	3.7	861	9	CC544845	CC544845 CH240_427
	32	38.8	3.7	562	6	CB495095	CB495095 omykswh00
	33	38.8	3.7	617	5	BP104977	BP104977 BP104977
	34	38.8	3.7	791	9	CC903578	CC903578 t007p04ba
c	35	38.8	3.7	830	9	CR070943	CR070943 Reverse s
c	36	38.8	3.7	847	9	CR267617	CR267617 Reverse s
c	37	38.8	3.7	849	9	CR258798	CR258798 Reverse s
	38	38.8	3.7	977	1	AL514490	AL514490 AL514490
	39	38.8	3.7	1101	3	CNS00ESU	AL069809 Drosophil
c	40	38.8	3.6	1843	9	AG435185	AG435185 Mus muscu
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c	42	38.6	3.6	1620	9	AG279955	AG279955 Mus muscu
	43	38.4	3.6	485	5	BP071285	BP071285 BP071285
	44	38.2	3.6	302	2	AU053798	AU053798 AU053798
	45	38.2	3.6	463	1	AU266721	AU266721 AU266721

ALIGNMENTS

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RESULT 1
CNS0187R
LOCUS       CNS0187R                 878 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108993
VERSION     AL108993.1   GI:5629297
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 878)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -.This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme/Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES            Location/Qualifiers
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                    /db_xref="taxon:7227"
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                    /clone_lib="DrosBAC"
                    /plasmid="pBeloBAC11"
                    /note="end : SP6"
ORIGIN

Query Match     4.2%;  Score 44.6;  DB 9;  Length 878;
Best Local Similarity  24.1%;  Pred. No. 0.69;
Matches  62;  Conservative  83;  Mismatches 112;  Indels  0;  Gaps  0;

Qy    762 ATAAGCATATACTGGACCATTGTAAAACCTGAGATATCCTAATGATAAACAGTAATGGC 821
          :|||.|.||::|:  .::: .|:::||.|:|:::.|:|:::.:|:.::: |.:| ||
Db     93 AWAAAMAWMMMAAAAAAAWWMAMARGAWAWGCWWGGAWWMMAWRGMMMWAWWAAAAAA 152
```

```
Qy   822  AACTTAGTTGCACCGCGGGGATATTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGA 881
               ::::: |||:|| : :  ::::|::::: :|| ::  :||::||
Db   153  WMMWCTTTGCMCTGAWTRTWGTTRTWTTWAWWWMRTTRAAWWWMAAWWWMAAWWWARGW 212

Qy   882  TCAGATGCGACCCATAGACATTTGTGTCTGAATGTATTACACCAAATGGAAGCATCCCC 941
               ::: |||:::  ::: :|||    || :||:||: :|:|||:
Db   213  WWRGMAAAARAWWMAMWRCRCWTWCRCMAAWMAAMAAAAMAMAAMARCAWWMMW 272

Qy   942  AACGACAACAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTATATC 1001
               :| :|||:  :: ::  :::||  |: : :| : |:|:| |||: |
Db   273  MAAMWCRAWMGGAWARAAWTRGAWWWMRAWMAAAMRARMAWRAWRMAAWAMAAWTWTA 332

Qy  1002  AGGCAAAACACTTTAAA 1018
               |||:|  |:|
Db   333  CAWAAAWAAAAARTMRTA 349
```

RESULT 2
AQ636729
LOCUS   AQ636729   598 bp   DNA   linear   GSS 17-JUN-1999
DEFINITION RPCI-11-477P23.TV RPCI-11 Homo sapiens genomic clone
            RPCI-11-477P23, genomic survey sequence.
ACCESSION   AQ636729
VERSION   AQ636729.1 GI:5099364
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 598)
AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
TITLE   Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
JOURNAL   Unpublished (1997)
COMMENT   Other_GSSs: RPCI-11-477P23.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES   Location/Qualifiers
     source   1..598
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="GDB:7683166"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-477P23"
                     /sex="Male"
                     /cell_type="lymphocytes"
                     /clone_lib="RPCI-11"
                     /note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
ORIGIN

Query Match   4.1%;   Score 43.8; DB 8; Length 598;
Best Local Similarity   56.4%; Pred. No. 1;
Matches 101; Conservative   0; Mismatches 77; Indels 1; Gaps 1;

Qy   100 ACACAGCCACATTATGTCTGGGACACCAGTAGCACCATGCAAATGGAACATTGGTAAAAACAA 159
               ||||| |||| |||: | ||||
Db   198 ATATAGCAGAAACACATTTATGACGATTACACATTATACAGAAAATGTTGACTAAAGAA 257
```

RESULT 3
CC081372/c
LOCUS       CC081372                 820 bp    DNA     linear   GSS 16-APR-2003
DEFINITION  CSU-K33r.31E9.SP6 CSU-K33r Aedes aegypti genomic clone
            CSU-K33r.31E9, genomic survey sequence.
ACCESSION   CC081372
VERSION     CC081372.1  GI:29929272
KEYWORDS    GSS.
SOURCE      Aedes aegypti (yellow fever mosquito)
ORGANISM    Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 820)
AUTHORS     Loftus,B., Shetty,J., Severson,D., Brown,S. and Knudson,D.
TITLE       End sequencing of Aedes aegypti BACs
JOURNAL     Unpublished (2003)
COMMENT     Other_GSSs: CSU-K33r.31E9.T7
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: enta@tigr.org
            Library was provided by Susan Brown and Dennis Knudson at Colorado
            State University.
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1..820
                     /organism="Aedes aegypti"
                     /mol_type="genomic DNA"
                     /strain="Rexville"
                     /db_xref="taxon:7159"
                     /clone="CSU-K33r.31E9"
                     /clone_lib="CSU-K33r"
                     /note="vector: pBeloBAC11; Site_1: HindIII"
ORIGIN

Query Match       4.1%;    Score 43.8;  DB 8;  Length 820;
Best Local Similarity   49.0%;  Pred. No. 1.1;
Matches  117;  Conservative   0;  Mismatches  122;  Indels  0;  Gaps  0;

```
Qy    42  ATTATTTTGATACTACTGACCCATTGGGTCTACAGTCTCAAAACCCAACCCAGTGGAAACAAC 101
               ||||||||||||||||| |     |||||   |||||||   |||| |||||
Db   284  ATCATTTCAAACCTGTTTTTCCGTTAGTTACACGGAAAATAAAATACGCTCCGAAAAAAA 225

Qy   102  ACAGCCACATTATGTCTGGGACACCAGTAGCACCATGCAAATGGAACATTGGTAAAAACAATA 161
               ||||||||||  |||||||||||   |||   ||||   |||  |||:||
Db   224  AAATAAAAATTTAATATTTTAAAAATAATAAAACCGAAAACAATTGAAATTTTTATTATTGCCAAA 165

Qy   162  ACTGATGACCAAATTGAGGTGACAAATGCTACTGAATTAGTTCAGAGCATTTCATAGGG 221
               |||||||||||||||||||||||||||||   ||| |||| |||||| ||||
Db   164  AATCAACAACTAGAAAAGGCTTCAAGAAAAAATGAAAAAAATGGATGTTCAAAATA 105

Qy   222  AAAATATGCAACAACTCATATAAAGTTCTAGATGGAAGAAGAATTGCACATTAATAGATGC 280
               |||||  |||| |||||||||||||||||||||||||||||||||||||
Db   104  AAAATTATAAAATCAAAATCAAAAATTTAAAAATTGTGAATAAAATTAATAAAAATGC 46
```

RESULT 4
CNS00905/c
LOCUS   CNS00905   854 bp   DNA   linear   GSS 03-JUN-1999

DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR19H07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL052980
VERSION   AL052980.1 GI:4934428
KEYWORDS   GSS.
SOURCE   Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 854)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cander Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES   Location/Qualifiers
     source   1..854
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR19H07"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

Query Match   4.0%; Score 42.8; DB 9; Length 854;
Best Local Similarity 30.3%; Pred. No. 2.1;
Matches 158; Conservative   2; Mismatches 358; Indels   3; Gaps   1;

Qy   536 AACAAAATCTGGAAACTTCTTACCCCACATTGAATGTGACAATGCCTAACAATAAAAATT 595
              || || ||||| ||||||||||||||||||||
Db   626 AAANAAAAAAANANANAAANANANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 567

Qy   596 CGACAAACTATACATCTGGGGGATTCATCACCCGAGCTCAAACCAACAGCAGACAGAATT 655
              || | ||||||| || ||||||||||||||
Db   566 AAANAANNNAAAAAAAANNNNNNAAAAAAANNNNNNNNAANNNANNAAAANANNANNNNN 507

Qy   656 GTACATCCAAGAATCAGGAGGACCAGGTAACAGTCTCAACAAAAGAAGTCAACAAACGATAGT 715
              | ||| || |||||||||||||||||||| ||||
Db   506 NNANANNNAAAANANAAANAANANAAAAAAAAAAAAAAAAAANNAANNANNAAANANNNAANNA 447

Qy   716 CCCTAATATCGGATCTAGACCGTGGGTTAGGGGTCAATCAGGCAGGATAAGCATATTACTG 775
              |||| ||| | ||||||||||||||||||
Db   446 NNNNAANANAAAANNNNAAAAAAAANNNAAANNNNAAANNNNNNAAAANA--ANNAAAAAAAAANNN 390

Qy   776 GACCATTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGCGAACTTAGTTGCACC 835
              |||| ||||| || |||||||||||||||||||||
Db   389 NNAAAANNAAAANNNNAAAAAAANNANNANANNANNAAAAAAAAAAAANNNAAAAANNNAAAAN 330

Qy   836 GCGGGGATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGATGCACCCAT 895
              | ||||| |||| || ||||||||||||||||
Db   329 NANAAAANAANNAAAAAAAAANATAAAAAANNNANNANNNNNNNNANNNNNNNANNNNNAN 270

Qy   896 AGACATTTGTGTGTCTGAATGTATTACCCAAATGGAGCATCCCCAAACGACAAACCATT 955
              | |||||| || |||||||||||
Db   269 ANNNANATNNNNNAAGNNNTANANNANNNAAAAAAAAAAAAAAAAAAAAAAAAANNNAAAANANA 210

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                                              956 TCAAAATGTGAACAAGTTACATATGGAAAATGTCCCCAAGTATATCAGGCAAAACACTT 1015
                                       Qy ||||||| ||||||||||||||||||
                                       Db   209 NNNNNANNAAAAANNNNNNNNNAAAAAAAAAAAAAAAAANNNNNAANANAAAANANNNNNNANN 150

                                       Qy   1016 AAAGCTGGCCACTGGGATGAGGAATATACCAGAAAAGCAAA 1056
                                                       | || |||||
                                       Db   149 NNNNCADVKAACCAAAAAGGAAAAAAANNNNNAAAAAABAA 109

RESULT 5
CNS0106X
LOCUS   CNS0106X   1101 bp   DNA   linear   GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL098595
VERSION   AL098595.1 GI:5611206
KEYWORDS   GSS.
SOURCE   Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1101)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES   Location/Qualifiers
     source   1..1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN03K20"
                     /clone_lib="DrosBAC"
                     /plasmId="pBeloBAC11"
                     /note="end : T7"
ORIGIN

Query Match   4.0%; Score 42.4; DB 9; Length 1101;
Best Local Similarity 19.3%; Pred. No. 3;
Matches   67; Conservative 140; Mismatches 141; Indels   0; Gaps   0;

Qy   563 ATTGAATGTGACAATGCCTAACAATAAAAATTTCGACAAACTATACATCTGGGGGATTCA 622
              ::::::::: :: : |||||::|||::::|:|:::||:|::|:::||::::::
Db   754 RDKRRWDAKKDKRKRAKAKAADDADADAKAADDADAKADADDGRGDGKKKRA 813

Qy   623 TCACCCGAGCTCAAACCAACAGCAGACAGAATTGTACATCCAAGAATCAGGAGGACGAGTAAC 682
              ::::::: :: |::|:|: :::|: |:|:: ||::| : : | :| ::| :
Db   814 KDRKKKKKDKAWGDKKCKAKKDKAAAKAKKDKAKRRAGDKDKAKADAKAAKKAK 873

Qy   683 AGTCTCAACAAAAGAAGTCAACAAACGATAGTCCCTAATATCGGATCTAGACCGTGGGT 742
              : ::| :: : |:|: ::: ::: : ||:|:|::| : : :| | ::| :: ::
Db   874 AKDDDDAKAATKAKKATKAKKKDKAKAKKKKKKDKAKAKAKAKDKDDKDKDKKK 933

Qy   743 TAGGGGTCAATCAGGCAGGATAAGCATATACTGGACCATTGTAAAACCTGGAGATATCCT 802
              ||| | ::: :|:::::: ::|:: ::::::|:: :::|::|:||::::||::|:|:: :
Db   934 DAKADKKKWKKDRAKDKAKKDDDKKDKAKDKDKDKDADAKWAKAKADADAKAKAKAKA 993

Qy   803 AATGATAAACAGTAATGGCAACTTAGTTGCACCGCGGGGATATTTTAAATTGAAAACAGG 862
              ::::|||||| ::: : |: :: : |: :: :::|::|: : :| :::::::|||| ||
Db   994 KAADDDAAADKAKAKADKAKADDAKAKAKAKADDADAKAKKAKRAAKRAAKADA 1053

```
Qy    863  GAAAAGCTCTGTAATGAGATCAGATGCACCCATAGACATTTGTGTGTC 910
           :||:|::.:::: .::::.:|:.:::.:|:::.    |.|::||.|.::.:::::
Db   1054  DAARAKAKADDKDKDAKKDDADKAKKAKAKAKDM 1101
```

RESULT 6
BY725844
LOCUS   BY725844   665 bp   mRNA   linear   EST 17-DEC-2002
DEFINITION   BY725844 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA
             clone B020021A19 5', mRNA sequence.
ACCESSION   BY725844
VERSION   BY725844.1 GI:27138971
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 665)
AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
             Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
             Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
             Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
             Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
             Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
             Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
             Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
             Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
             Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
             Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
             Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
             Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
             Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
             Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
             Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
             Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
             Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tonita,M.,
             Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
             Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
             Yang,L., Yuan,J., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
             Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
             Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
             Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
             Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
             Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
             Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE   Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
MEDLINE   22354683
PUBMED   12466851
COMMENT   Contact: Yoshihide Hayashizaki
             Laboratory for Genome Exploration Research Group, RIKEN Genomic
             Sciences Center(GSC), Yokohama Institute
             The Institute of Physical and Chemical Research (RIKEN)
             1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
             Tel: 81-45-503-9222
             Fax: 81-45-503-9216
             Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
             Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
             Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
             Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
             Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
             Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
             Sano,H., Sasaki,D., Sato,O., Shibata,K., Shiraki,T., Tagami,M.,
             Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
             Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
             Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new
             genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
             encyclopedia: real-time sequence clustering for construction of a
             nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
             further details.
FEATURES   Location/Qualifiers
     source   1..665
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="B020021A19"
                     /tissue_type="egg"
                     /dev_stage="2 cells"
                     /clone_lib="RIKEN full-length enriched, 2 cells egg"
                     /note="Site 1: Sall; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAAGGAGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCGAGTAATTAAATTAAATCCCCCCCCCC 3'], cDNA
                     was cleaved with XhoI and BamHI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match   4.0%; Score 42; DB 6; Length 665;
Best Local Similarity 50.0%; Pred. No. 3.3;
Matches 105; Conservative   0; Mismatches 105; Indels   0; Gaps   0;

```
Qy    819  GGCAACTTAGTTGCACCGCGGGATATTTAAAATTGAAAACAGGGAAAAGCTCTGTAATG 878
           |||:||| ||||| |||||||  |||||| ||||||  |||||||  |||||||||
Db    177  GACAAACCAAATGAACTGTGTGGTTCATCTCATGTGCCCAGAGGTGGAAACTCGACCCAT 236

Qy    879  AGATCAGATGCACCCATAGACATTTGTGTGTCGAATGTATTACCCAAATGGAAGCATC 938
           |||| |||||||||||||||  ||||||||| |||||| ||| || ||||||||||||
Db    237  ATATCTCATCCACCCTGACAAATAATTGATTCAGAATGATGGATCACCCGCCATTGATAGAAGA 296

Qy    939  CCCAACGACAAACCATTTCAAAATGTGAACAAAGTTACATATGGAAAATGCCCCAAGTAT 998
           |||:||  ||||||||| |||||||||||||| ||||| ||||||||||||||||||||
Db    297  CCAGAAGCTCTGAAACTGCAGGATGAGAACAAAGAATAAATGCTAGATAGATTCATGAAA 356

Qy    999  ATCAGGCAAAACACTTTAAAGCTGGCCACT 1028
           ||||||||||||||| |||| |||| ||||
Db    357  AGGACTCCAGGAATTTAGATGGTGGTCATT 386
```

RESULT 7
CNS00LRE/c
LOCUS   CNS00LRE   1106 bp   DNA   linear   GSS 14-JUN-1999
DEFINITION   Drosophila melanogaster genome survey sequence T7 end of BAC:
             BACR48P05 of RPCI-98 library from Drosophila melanogaster (fruit
             fly), genomic survey sequence.
ACCESSION   AL078654
VERSION   AL078654.1 GI:5101944
KEYWORDS   GSS.
SOURCE   Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
             Ephydroidea; Drosophilidae; Drosophila.

REFERENCE   1 (bases 1 to 1106)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp; cn bw sp, the same strain used for the P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
        source   Location/Qualifiers
                  1..1106
                  /organism="Drosophila melanogaster"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:7227"
                  /clone="BACR48P05"
                  /clone_lib="RPCI-98"
                  /note="end : T7"
ORIGIN

Query Match   3.9%; Score 41.6; DB 9; Length 1106;
Best Local Similarity   15.4%; Pred. No. 5;
Matches   55; Conservative 151; Mismatches 152; Indels   0; Gaps   0;

Qy   588 AAAAATTTCGACAAACTATATACATCTGGGGATTCATCACCGAGCTCAAACCAACAGCAG 647
              :::   ::::   ::   ::::   :   : : :: : :::::|::|:
Db   1041 AHHHDKRSNKKBDGDSVNTMVADNTBWSRRRHCNVRBDSCSMVHAWVTDYBCRCNYTKWG 982

Qy   648 ACAGAATTGTACATCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAAGTCAACAA 707
              :::::|:::: :::   :: || : :||| :|::|:|:|||:|| | | ||
Db   981 VSWKWBTBKHYVMBCBYKWBWHAAAWAWWAADAACCCRBRWVAVAWAAMRAMRMAAAAA 922

Qy   708 ACGATAGTCCCTAATATCGGATCTAGACCCGTGGGTTAGGGGTCAATCAGGCAGGATAAGC 767
              :   :: : ::: :: :|:|:|::|:|||:::||:|| :|:|| |:|:|:|::
Db   921 MKHTSGBKYKTSYYDMHHTKYKWKHRWYWYKSGNGGSHSGGSMVAWCMRHAYTHRKVWYYW 862

Qy   768 ATATACTGGACCATTGTAAAACCTGGAGATATCCTAATGATAAACAGTAATGGCAACTTA 827
              :::::::|::|:   :: ||:|:::: :: | ::|:| :::|:||:
Db   861 NWWBDSDGBVCMCCVMAHWCAHBMVHCYYNAMSCANBAWYVAWKSBTRMTHAWNWYTCA 802

Qy   828 GTTGCACCGCGGGGATATTTTAAATTGAAAACAGGGAAAAGCTCTGTAATGAGATCAGAT 887
              :::|:|:::|:: ||: :: : ::   : :::: : ::: :::::|:|
Db   801 ANGNTKWARSGSGCACCSBGMRHYTGGGGRARSGGKMGMVCRCCVKBWMAHBHNBWHNNY 742

Qy   888 GCACCCATAGACATTTGTGTGTCTGAATGTATTACCACCAAATGGAAGCATCCCCAACG 945
              :|:|:::| :||:||:: ||::: | ::: :::::|::|:::|::|:||:|::|:|
Db   741 NNMAMAMAAVAMMNWATKYKKNACYYKTGDVAYMMRAVARCSHRVMNCVAVAVAWABG 684

RESULT 8
AQ055729/c
AQ055729
LOCUS   AQ055729   733 bp   DNA   linear   GSS 30-JUL-1998
DEFINITION CIT-HSP-2341D11.TF CIT-HSP Homo sapiens genomic clone 2341D11, genomic survey sequence.
ACCESSION   AQ055729
VERSION   AQ055729.1 GI:3352335
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 733)

AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE   Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
JOURNAL   Unpublished (1998)
COMMENT   Other GSSs: CIT-HSP-2341D11.TR
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES
        source   Location/Qualifiers
                  1..733
                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
                  /clone="2341D11"
                  /sex="Male"
                  /cell_type="Sperm"
                  /clone_lib="CIT-HSP"
                  /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
ORIGIN

Query Match   3.9%; Score 41.4; DB 8; Length 733;
Best Local Similarity   53.4%; Pred. No. 5;
Matches   87; Conservative   0; Mismatches 76; Indels   0; Gaps   0;

Qy   129 GCAGTAGCAAATGGAACATTCGTAAAACATAACTGATGACCAAATTGAGGTGACAAAT 188
              |||| |||||| || || | ::| | ::|||:||||||||:|||||:|||||
Db   469 GCAGCAGGAAATGAAATGAATGATTAAATTAAAAGAAGAGAAAAAATATCAATAGTAGTTT 410

Qy   189 GCTACTGAATTAGTTCAGAGCATTTCAATAGGAGAAAATATGCAACAACTCATATAAAGTT 248
              | ::: ||| ||||||||| |:|:||| | ||||| :: |:| ::|::||||||:
Db   409 TAAAATAAATATGTTCAGAAAATCTGAAAGGGTAAAAAATGAATAAAATCCATAAAAGGAA 350

Qy   249 CTAGATGGAAGAAATTGCACATTAATAATGATAGATGCAATGCTAGGAG 291
              | ||::|:|:|||| ||:|:|||||| || :: |||:|:||||:|||||
Db   291 CTAGATGGAAGAAATTGCACATTAATAATGATAGATGCAATGCTAGGAG 291

Qy   349 CAAGAAATTATGAACTAAAGCAGCAGTTAAAATGAAATAATAAAAG 307
Db   307

RESULT 9
CNS00H6Y
LOCUS   CNS00H6Y   1101 bp   DNA   linear   GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC: BACR34L01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION   AL073010
VERSION   AL073010.1 GI:4952872
KEYWORDS   GSS.
SOURCE   Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1101)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES   Location/Qualifiers
     source   1..1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR34L01"
                     /clone_lib="RPCI-98"
                     /note="end : T7"

ORIGIN

Query Match   3.9%;   Score 41; DB 9; Length 1101;
Best Local Similarity 43.1%; Pred. No. 7.3;
Matches 119; Conservative 13; Mismatches 144; Indels 0; Gaps 0;

Qy   79 AAAACCCACCAGTGGAAACAACACAGCCACCATTATGTCTGGGACACCATGCAGTAGCAA 138
         || ||||| | |||||||||||||||||||||
Db   302 AACCCCCATCCAATCAATCAATNCCTTACATAAATTAAACTAATCACAACACAACAAA 361

Qy   139 ATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAAT 198
         |||||||||| | | | |||||| ||:||||||||||
Db   362 TACAAACAAAWACACCAAAWATATTTATATATATAATATAWATTAAAAAATCCACATT 421

Qy   199 TAGTTCAGGCATTTCAATAGGGAAAAATGCAACAACTCATATAAAGTTCTAGATGGAA 258
         ||| | |||| ||| |||:|||||||
Db   422 CAATACCAATATATAATATATTCCCYATATTCACATACACATATCATATATATACAA 481

Qy   259 GAAATTGCACATTAATAGATGCATGCTAGGAGACCCCCACTGTGATGTCTTCCAGTATG 318
         |||||||:: || || |||| |
Db   482 CMAATTRSGCCTKTTTAAACTCTTTTCSAATASGCGCCCATKTSCAAGGAATTKCAAACTC 541

Qy   319 AGAATTGGGACCTCTTCATAGAAAGAAGCAGCGCTT 354
         |:||||:| | | :| |:|||
Db   542 AGACTTGSGAGAACAASAATTAGRSAGCAASATCAT 577

RESULT 10
AG429915/c
LOCUS   AG429915   1362 bp   DNA   linear   GSS 03-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-304L12.TJ, genomic survey
            sequence.
ACCESSION   AG429915
VERSION   AG429915.1 GI:48072978
KEYWORDS   GSS.
SOURCE   Mus musculus molossinus
  ORGANISM Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE   BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1362)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT   Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector   : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES   Location/Qualifiers
     source   1..1362
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-304L12.TJ"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match   3.9%;   Score 41; DB 9; Length 1362;
Best Local Similarity 34.2%; Pred. No. 7.7;
Matches 179; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

Qy   536 AACAAAATCTGGAAACTCTTACCCCACATTGAARTGTGACAATGCTAACATAAAAAATTT 595
         || ||| | |||||||||||||||||||||||
Db 1086 AAAANNAANAAAAAANNANNAAAAAAAAAAAANNNANAAAAAANNANAAAAAAAAAA 1027

Qy   596 CGACAAACTATACATCTGGGGGATTCATCACCCGAGTCTCAAACCAACGACAGCAGAATT 655
         |||| |
Db 1026 AAAAAAANAANAAAAAAAAANANNNNAANNANNNANANNNNNANANAAAAAAAAAA 967

Qy   656 GTACATCCAAGAATCAGGACGAGTAACAGTCTCAACAAAAGAGTCAACAAACGATAGT 715
         |||||||||| || |||||||||||||||||
Db   966 AAANANNNAAAANNNAAAANNNAAAAAAAAAAAAAAAAANNNNNAAAAA 907

Qy   716 CCCTAATATCGGATCTAGACCGTGGGTGGTTAGGGGTCAATCAGGCAGGGATAAGCATATACTG 775
         |||| ||||||||||||
Db   906 AAAAAAAANNANNNAANNANANAAANANNANNNNAANNAAAAANNNNNAANAAAAAANNN 847

Qy   776 GACCATTGTAAAACCTGGACATATCCTAATGATAAACAGTAATGGCAACTTAGTTGCACC 835
         ||||||||||||
Db   846 NAANAAAAAAAAANNNAAAAANNNNNAAAAANNNAAAANNNAAAANNAAAANAAAAAN 787

Qy   836 GCGGGGATATTTTAAATTGAAAACAGGGAAAAGTCTCGTAATGAATCAGATGCACCCAT 895
         |||| |||
Db   786 ANAAANAAAAANNAAAAAAAAAAANNAAAAAAAANNNNNAAAAANNNAAAAAANNAA 727

Qy   896 AGACATTTGTGTCTGAATGTATTACACACAAATGGAAGCATCCCAACGACAAACCATT 955
         |||| ||||
Db   726 AAAAANAAAANNNANNAAAANAANNNANNANNNANNAAAAANNANNANNNAANANANA 667

Qy   956 TCAAAATGTGAACAAAGTTACATATGGAAAATGCCCCAGTATATCAGGCAAAACACTTT 1015
         || ||||||
Db   666 AAAAAAANNAANNAAANNANAAANANANNANNNNAANNANNNAAANAANAAAAAANAA 607

Qy 1016 AAAGCTGGCCACTGGGATGAGGAATATACCAGAAAAGCAAATCA 1059
         |||| |||||||||||
Db   606 NAANNNAAAAAANNNNNAAANNNNNAAANNAAAANAAAAAAANANA 563

RESULT 11
BX69329S/c
LOCUS   BX69329S   879 bp   mRNA   linear   EST 14-NOV-2003
DEFINITION BX69329S XGC-neurula Xenopus tropicalis cDNA clone TNeu103g10 3',
            mRNA sequence.
ACCESSION   BX69329S
VERSION   BX69329S.1 GI:38342415
KEYWORDS   EST.
SOURCE   Xenopus tropicalis (western clawed frog)
  ORGANISM Xenopus tropicalis

REFERENCE
AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE   Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL   Unpublished (2003)
COMMENT   Contact: Croning MDR
           Sanger Institute
           Hinxton, Cambridgeshire, CB10 1SA, UK
           Email: trop@anger.ac.uk
           Sanger Xenopus tropicalis EST project 2001
           TROPICALIS_SEQUENCE_ID: TNeu103g10.q1kT7
           Sequencing primer: T7
           This sequence is from a Xenopus Gene Collection (XGC) library
           constructed by Aaron M. Zorn.
           cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
           EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
           5' end and NotI at the 3' end.
           Vector: pCS107; Site_1: EcoRI; Site_2: NotI
           Host: Escherichia coli DH10B.
FEATURES   Location/Qualifiers
     source   1..879
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TNeu103g10"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /clone_lib="XGC-neurula"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
ORIGIN
     Query Match   3.8%; Score 40.8; DB 5; Length 879;
     Best Local Similarity 54.7%; Pred. No. 7.7;
     Matches 81; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy   88 CCAGTGGAAACAACACAGCCACATTATGTCTGGGACACCATGCAGTAGCAAATGGAACAT 147
          | ||| |||| ||| || || |||| | ||| || ||| | ||| ||||| ||||||
Db   153 CCTCTTGAACCTACTGCGCCCCATTGTTCTGTCGAGACCAAGTAGCCTCAAACCACTTCT 94

Qy   148 TGGTAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTACTGAAGTTAGTTCAGA 207
          | ||||| || ||| ||||| |||||| ||||| ||| ||||| || |||||| |||||
Db   93 TCCTGACAATATGACTTGATGGCCCAACAAAATGTGACCACTAAATCATTAAAATAAAA 34

Qy   208 GCATTTCAATAGGGAAAAATGCAACAA 235
          | ||||| |||| |||| |||| ||||
Db   33 GCACTTTAATATAAAAAAAAAAAAAAA 6

RESULT 12
CL650318/c
LOCUS   CL650318   1342 bp   DNA   linear   GSS 06-JUL-2004
DEFINITION CH213-288A10.T7 CH213 Gasterosteus aculeatus genomic clone
           CH213-288A10 5', genomic survey sequence.
ACCESSION CL650318
VERSION   CL650318.1 GI:49669742
KEYWORDS   GSS.
SOURCE   Gasterosteus aculeatus
ORGANISM   Gasterosteus aculeatus (three spined stickleback)
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
           Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
           Gasterosteidae; Gasterosteus.
REFERENCE 1 (bases 1 to 1342)
AUTHORS   Kingsley,D., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
TITLE   Expressed sequence tags from Gasterosteus aculeatus
JOURNAL   Unpublished (2004)
COMMENT   Contact: Grimwood, Jane
           Stanford Human Genome Center

           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
           Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 879)

COMMENT   Stanford University School of Medicine
           975 S California Avenue, Palo Alto, CA 94304, USA
           Tel: 650 320 5917
           Fax: 650 320 5801
           Email: jane@shgc.stanford.edu
           Plate: 288
           Class: BAC ends
           High quality sequence start: 24
           High quality sequence stop: 451.
FEATURES   Location/Qualifiers
     source   1..1342
                     /organism="Gasterosteus aculeatus"
                     /mol_type="genomic DNA"
                     /strain="Salmon River"
                     /db_xref="taxon:69293"
                     /clone="CH213-288A10"
                     /sex="Mixed"
                     /cell_type="Blood"
                     /clone_lib="CH213"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; The sequence of
                     the clone was established as a mapping and sequencing
                     collaboration at the Stanford Genome Evolution Center,
                     funded by the NIH Centers of Excellence in Genomic Science
                     (CEGS) initiative (http://cegs.stanford.edu). The clone
                     was isolated from the BAC library CHORI-213 built by
                     Pieter deJong in collaboration with the Stanford Genome
                     Evolution Center (http://www.chori.org/bacpac/). Clones
                     may be purchased from BACPAC Resources
                     (http://www.chori.org/bacpac/ordering_information.htm)."
ORIGIN
     Query Match   3.8%; Score 40.8; DB 9; Length 1342;
     Best Local Similarity 52.3%; Pred. No. 8.7;
     Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy   134 AGCAAATGGAACATTGGTAAAAACAATAACTGATGACCAAATTGAGGTGACAAATGCTAC 193
          ||||| ||||| ||||| |||| || ||| ||||| |||||| ||||| ||||
Db   1075 AGCTAATGAAAAGTTTATAAAATAAAAAGATGTAAGAGTGATAAGGTATAAGATTTAAT 1016

Qy   194 TGAATTAGTTCAGAGCATTTCAATAGGGAAAAATGCAACAACTCATATAAAGTTCTAGA 253
          | ||| || |||||| ||||| |||| |||| |||| |||| ||| || ||||
Db   1015 TAAAGAAATTATAAGTAAAGAAATGAAATGAAATGATAATATAAAAGCTATTAAAATTGTAAA 956

Qy   254 TGGAAGAAATTGCACATTAATAGATGCAATGCTAGGAGACCCCCACTGTGAT 305
          | |||||||| |||| || || |||| |||| |||| |||| ||||
Db   955 TTAAATTAATAGTAAATATTTAGAGAAAATGATAAGAGAAATAGAGTATGGT 904

RESULT 13
BH744818
LOCUS   BH744818   503 bp   DNA   linear   GSS 25-FEB-2002
DEFINITION gt42d05.b1 BoBuds01 Brassica oleracea genomic clone gt42d05 5',
           genomic survey sequence.
ACCESSION BH744818
VERSION   BH744818.1 GI:18879572
KEYWORDS   GSS.
SOURCE   Brassica oleracea
ORGANISM   Brassica oleracea
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 503)
AUTHORS   Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J.,
           Balija,V., Cunnius,D.M., Katzenberger,F., King,L., Kirchoff,K.,
           Kuit,K., Miller,B., Muller,S., Nascimento,L., Preston,R.,
           Santos,L., Shah,R., Zutavern,T., Dedhia,N., Rabinowicz,P.D. and
           McCombie,W.R.
TITLE   Whole Genome Shotgun Reads from Brassica oleracia (2002b)
JOURNAL   Unpublished (2002)
COMMENT   Contact: W. Richard McCombie
           Lita Annenberg Hazen Genome Sequencing Center
           Cold Spring Harbor Laboratory
           PO Box 100, Cold Spring Harbor, NY 11724, USA

```
          Tel: 516 367 8884
          Fax: 516 367 8874
          Email: mccombie@cshl.org
          Plate: gt42 row: d column: 05
          Seq primer: -21UnivFwd
          Class: shotgun
          High quality sequence stop: 503.

FEATURES             Location/Qualifiers
     source          1..503
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="gt42d05"
                     /clone_lib="BoBuds01"
                     /note="Vector: M13 for .x reads, pBluescript for .b and .g
                     reads; Site 1: EcoRV; Whole genome shotgun library from
                     flowering buds. DNA was purified from a crude nuclear prep
                     using Brassica oleracea TO1000DH3 buds provided by Thomas
                     Osborn at the University of Wisconsin. Genomic DNA
                     provided by Pablo Rabinowicz (CSHL) and shotgun library
                     prepared in McCombie Lab."

ORIGIN

Query Match             3.8%; Score 40.6; DB 8; Length 503;
Best Local Similarity 58.8%; Pred. No. 7.4;
Matches  70; Conservative  0; Mismatches 49; Indels  0; Gaps  0;

Qy  187 ATGCTACTGAATTAGTTCAGAGACATTCAGAGACATTAATAGATGCAATGCAACACTCATATAAAG 246
        |||||      ||||| |||||||   |||||  | ||  |||| | ||| | ||| | ||| ||
Db  365 ATGGCTTTGAATTACCTGTGATTAATTCAATAGTGAAAAGAGATCTAGAGTAAGATCCAG 424

Qy  247 TTCTAGATGGAAGAAATTGCACATTAATAGATGCAATGCAATGCCCCACTGTGAT 305
        || | || ||||| || || || || ||||| ||  ||| |  |||
Db  425 CTAAAAGGAAAAGTAGAACATTCAGACATGAAGTCTACGGAGGAACAAACTCTTAT 483

RESULT 14
LOCUS       CK563538
DEFINITION  rswpb0 006755.y1 swp Bombyx mori cDNA, mRNA sequence.
            643 bp    mRNA    linear    EST 05-OCT-2004
ACCESSION   CK563538
VERSION     CK563538.1  GI:40947992
KEYWORDS    EST.
SOURCE      Bombyx mori (domestic silkworm)
ORGANISM    Bombyx mori
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
            Bombycoidea; Bombycidae; Bombyx.
REFERENCE   1 (bases 1 to 643)
AUTHORS     Xia,Q., Zhou,Z., Lu,C., Cheng,D., Dai,F., Li,B., Zhao,P., Zha,X.,
            Cheng,T., Chai,C., Pan,M., Li,C., Liu,C., Lin,Y., Qian,J., Hou,Y.,
            Wu,Z., Li,G., Pan,M., Li,C., Shen,Y., Lan,X., Yuan,L., Li,T.,
            Xu,H., Yang,G., Wan,Y., Zhu,Y., Yu,M., Shen,W., Wu,D., Xiang,Z.,
            Yu,J., Wang,J., Li,R.Q., Shi,J.P., Li,H., Li,G.Y., Su,J.N.,
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            Xu,J.Z., Sun,H.B., Dong,L., Liu,D.Y., Zhao,S.L., Zhao,X.L.,
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            He,D.D., Huang,H.Y., Zhang,X.W., Wang,Z.Q., Li,W.J., Cao,Y.Z.,
            Zhang,H.K., Ye,J., Ji,H., Li,S.T., Ni,P.X., Zhang,J.G., Zhang,Y.,
            Zheng,H.K., Ye,J., Wang,J., Wong,G.K.S. and Yang,H.M.
TITLE       A draft sequence for the genome of the domesticated silkworm
            (Bombyx mori)
JOURNAL     Unpublished (2004)
COMMENT     Contact: Zhonghuai Xiang
            Southwest Agricultural University
            Chongqing Beibei
            Tel: 86-23-68251123
            Fax: 86-23-68251128
            Email: xzh@swau.cq.cn.
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DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
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ACCESSION   AL107506
VERSION     AL107506.1  GI:5627693
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Drosophila melanogaster
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REFERENCE   1 (bases 1 to 968)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
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